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OM nucleic - nucleic search, using bw model

Run on: February 12, 2004, 01:54:29 ; Search time 615.146 Seconds
(without alignments)
1396.582 Million cell updates/sec

Title: US-09-692-077D-13

Perfect score: 21
Sequence: 1 gctcatcacccttcctcgct 21

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 2888711 seqs, 2045481386 residues

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-Processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

GeneBml:*
1: gb_ba:*
2: gb_hcg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pac:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sce:*
12: gb_ey:*
13: gb_un:*
14: gb_vl:*
15: em_ba:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
20: em_om:*
21: em_or:*
22: em_ov:*
23: em_pac:*
24: em_ph:*
25: em_pl:*
26: em_ro:*
27: em_sce:*
28: em_un:*
29: em_vl:*
30: em_hcg_hum:*
31: em_hcg_inv:*
32: em_hcg_other:*
33: em_hcg_mus:*
34: em_hcg_pin:*
35: em_hcg_rtd:*
36: em_hcg_mam:*
37: em_hcg_vtc:*
38: em_ey:*
39: em_hcgo_hum:*
40: em_hcgo_mus:*
41: em_hcgo_other:*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	21	100.0	21	6 AX350501	AX350501 Sequence
2	21	100.0	1149	4 AP337539	AP337539 Peroprus
3	21	100.0	1149	4 RAM315937	AJ315937 Roussetus
4	21	100.0	1150	4 CSE251181	AJ251181 Cynopteru
5	21	100.0	1156	4 MIA251107	AJ251107 Microptera
6	21	100.0	1162	4 FCA251174	AJ251174 Felis cat
7	21	100.0	1167	4 AP337538	AF337538 Hippodide
8	21	100.0	1167	4 NAL419805	AJ419805 Nyctimene
9	21	100.0	1167	4 RCR419806	AJ419806 Rhinoloph
10	21	100.0	1168	4 PVI251176	AJ251176 Phoca vit
11	21	100.0	1170	4 AP337543	AF337543 Taphozous
12	21	100.0	1171	4 DDAR28	Y15947 Dugong dugo
13	21	100.0	1171	4 TMA251109	AJ251109 Trichechu
14	21	100.0	1171	9 CVA251182	AJ251182 Cynoceph
15	21	100.0	1172	10 ARU427256	AJ27256 Apidomoni
16	21	100.0	1173	4 APA419813	AJ419813 Antrozous
17	21	100.0	1173	4 EAT419810	AJ419810 Emballionu
18	21	100.0	1174	4 PCA427417	AJ427417 Physeter
19	21	100.0	1176	4 AP337537	AF337537 Megaderma
20	21	100.0	1176	4 AP337542	AF337542 Tadartida
21	21	100.0	1176	4 LAL315940	AJ315940 Lagenorhy
22	21	100.0	1176	4 NMO427255	AJ427255 Marmota m
23	21	100.0	1176	10 SVU315942	AJ315942 Sciurus v
24	21	100.0	1177	4 BPH251175	AJ251175 Balaeonot
25	21	100.0	1177	4 BPAR28	Y15944 Bos taurus
26	21	100.0	1179	4 AP337540	AF337540 Myotis da
27	21	100.0	1180	4 LPA505821	AJ505821 Lama paco
28	21	100.0	1180	4 MCA251180	AJ251180 Macroctus
29	21	100.0	1180	9 NCO251186	AJ251186 Nycticebu
30	21	100.0	1185	10 ASP427259	AJ427259 Anomaluru
31	21	100.0	1185	10 GGL427258	AJ427258 Gliis glis
32	21	100.0	1194	4 SCT315936	AJ315936 Sorex cin
33	21	100.0	1197	4 LPA315941	AJ315941 Lama paco
34	21	100.0	1197	4 MTE505820	AJ505820 Manis tel
35	21	100.0	1203	10 DME427261	AJ427261 Dipodomys
36	21	100.0	1344	6 AX350490	AX350490 Sequence
37	21	100.0	1344	9 AP316895	AF316895 Homo sapi
38	21	100.0	1353	6 AX350489	AX350489 Sequence
39	21	100.0	2072	6 AR270618	AR270618 Sequence
40	21	100.0	2072	9 HUMADR28RA	M34041 Human alpha
41	21	100.0	3274	6 AX548756	AX548756 Sequence
42	21	100.0	6904	6 AX344977	AX344977 Sequence
43	21	100.0	6904	6 AX348498	AX348498 Sequence
44	21	100.0	9842	9 AF005900	AF005900 Homo sapi
45	21	100.0	22842	9 AC092603	AC092603 Homo sapi

ALIGNMENTS

RESULT 1	AX350501	21 bp	DNA	linear	PAT 06-FEB-2002
LOCUS	Sequence 13 from Patent WO0179561.				
ACCESSION	AX350501				
VERSION	AX350501.1	GI:18616097			
KEYWORDS					
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
REFERENCE	Ligett,S.B. and Small,K.M.				
AUTHORS	Alpha-2 adrenergic receptor polymorphisms				
TITLE	Patent: WO 0179561-A 13 25-OCT-2001;				
JOURNAL					

Query Match	100.0%;	Score 21;	DB 4;	Length 1149;
Best Local Similarity	100.0%;	Pred. No. 18;		

CSP251181		1150 bp	DNA	linear	MAM 01-JUN-2001
Cynopneuste sphinx partial dar2b gene for alpha adrenergic receptor					
B.					
AJ251181					
CCESSION					
VERSION					
AJ251181.1	GI:	11322256			

KEYWORDS	aar2B gene; alpha adrenergic receptor 2B.
SOURCE	Cynoporus sphinx (Indian short-nosed fruit bat)
ORGANISM	Cynoporus sphinx Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Chiroptera; Megachiroptera; Pteropodidae; Pteropodinae; Cynoporus.
REFERENCE	1 Madsen, O., Seally, M., Douady, C.J., Kao, D.J., Debry, R.W., Adkins, R., Amarine, H.M., Stanhope, M.J., de Jong, W.W. and Springer, W.S. Parallel adaptive radiations in two major clades of placental mammals <i>Nature</i> 409 (6820), 610-614 (2001)
JOURNAL	21082081
MEDLINE	11214318
PUBMED	2 (bases 1 to 1150)
REFERENCE	Madsen, O. Direct Submission Submitted (18-NOV-1999) Madsen O., Department of Biochemistry, University of Nijmegen, P.O. box 9101, 6500 HB Nijmegen, NETHERLANDS
TITLE	Location/Qualifiers
FEATURES	1..1150 /organism="Cynoporus sphinx" /mol_type="genomic DNA" /db_xref="taxon:9400" 1..1150 /gene="aar2B" <1..>1150 /gene="aar2B" /codon_start=2 /product="alpha adrenergic receptor 2B" /protein_id="CAC16684.1" /db_xref="GI:1132257" /db_xref="SPTRMBL:Q9GL20" translation="AAIAVIFELITFTFGNALVTILAVLTFRSLRAPONLPLVLSAA DLVATLIIPSLANELLGWYFRRTECVYLADVAFCSSIVHLCASIDRYAVVS RALEYNKRTPRRIKICILITYTLWAIVYSLPULYKDGQGPHGACOCKINQOANTYT LASTSGFPAPRLIMLVLYRTYLIARSHRGPRAGGLDSSKKOPHRVPGGPSTLL ASCIPASGEARPSRKPTGEKEQGETDEGSPALPSPMPALPHGSSPKFAVCVSLSE EIGEEDCECEFOALPASPASCSPPROPOQSRLVATLRGVLLGKGIGTGCGMMRRR RAQLTRESRFVFVLAIVGVFLCMFPFFFSYSLGALCPGRCKVPHGLF"
BASE COUNT	181 a 395 c 337 g 237 t
ORIGIN	
Query Match	100.0%; Score 21; DB 4; Length 1150;
Best Local Similarity	100.0%; Pred. No. 18;
Matches	21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY	1 GCTCATCATCCCTTTTCGCT 21
Db	151 GCTCATCATCCCTTTTCGCT 171
RESULT 5	
LOCUS	MLA251107 1156 bp DNA linear MAM 15-NOV-2000
DEFINITION	Microptomogale lamottei partial aar2B gene for alpha adrenergic receptor.
ACCESSION	AJ251107
VERSION	AJ251107.1 GI:11191767
KEYWORDS	aar2B gene; alpha adrenergic receptor; subtype 2B.
SOURCE	Microptomogale lamottei (Nimba otter shrew)
ORGANISM	Microptomogale lamottei Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Insectivora; Tenrecidae; Potamogalinae; Microptomogale.
REFERENCE	1 van Dijk, M.A.M., Madsen, O., Catzeffis, F., Stanhope, M. and de Jong, W.W. Probing 1the protein sequence support for the 'African clade' of mammals unpublished 2 (bases 1 to 1156)
TITLE	
JOURNAL	
REFERENCE	

FEATURES	source
gene	1. .1156 /organism="Micropterus dolomieu lamottei" /mol_type="genomic DNA" /db_xref="taxon:105689"
CDS	1. .1156 /gene="aar2B" /locus_tag="aar2B" /codon_start=2 /product="alpha adrenergic receptor, subtype 2B" /protein_id="CAC16396.1" /db_xref="GI:1191768" /translation="ATAAATTTTTLTILPFGNALVTLVLTSLRSLAPONFLVSLAAADIVATLITRPSLANELGWYRRHTRCEYLLADVLFCSSIVHLCAISLDRWAVSLAEVSGKTPRIRIKCHILITLWVLAIAISLPLTKDDQSPQPHGRQCKLNDQAMVITLSSISGFFAPACIMITLVLRILYLAIRSSRCRGPSSKGRSGVGRKQPHPLAAGTSLAKSTLTSLVAVGEANAGSGKSPGEGEETKDPVAPLPPNMAAHPHSGIGQKGGCTSPPEEBAEEECGPOAVASPASGSPLOOPRGRVLTATRGVTLISRGGAACGGQMMWRRTTOLTRERGRFTFVAVIGVYVLCMPFFPSISLGLCPQKCKVHGLF"
BASE COUNT	176 a 411 c 339 g 230 t
ORIGIN	
Query Match	100.0%; Score 21; DB 4; Length 1156;
Best Local Similarity	100.0%; Pred. No. 18;
Matches	21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	1 GCTCATCATCCCTTTCGCT 21 151 GCTCATCATCCCTTTCGCT 171
RESULT 6	
LOCUS	FCa251174 1162 bp DNA linear MAM 01-JUN-2001
DEFINITION	Felis catus partial aar2B gene for alpha adrenergic receptor 2B.
ACCESSION	AJ251174
VERSION	AJ251174.1 GI:11322248
KEYWORDS	aar2B gene; alpha adrenergic receptor 2B.
ORGANISM	Felis catus
REFERENCE	1 Madsen, O.; Scallan, M.; Donady, C. J.; Kao, D. J.; DeBry, R. W.; Adkins, R.; Amrine, H. M.; Stanhope, M. J.; de Jong, W. W. and Springer, M. S. Parallel adaptive radiations in two major clades of placental mammals
AUTHORS	Madsen, O., Scallan, M., Donady, C. J., Kao, D. J., DeBry, R. W., Adkins, R., Amrine, H. M., Stanhope, M. J., de Jong, W. W. and Springer, M. S.
TITLE	Parallel adaptive radiations in two major clades of placental mammals
JOURNAL	Nature 409 (6820), 610-614 (2001)
MEDLINE	21082081
PUBMED	11214318
REFERENCE	2 (bases 1 to 1162)
AUTHORS	Madsen, O.
TITLE	Direct Submission
JOURNAL	Submitted (18-NOV-1999) Madsen O., Department of Biochemistry, University of Nijmegen, P.O. box 9101, 6500 HB Nijmegen, NETHERLANDS
FEATURES	Location/Qualifiers
source	1. .1162 /organism="Felis catus" /mol_type="genomic DNA" /db_xref="taxon:9685" 1. .1162 /gene="aar2B" /locus_tag="aar2B" /db_xref="taxon:9685" 1. .1162 /codon_start=2 /product="alpha adrenergic receptor 2B"

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 /db_xref="GI:11322249"
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 LASSIGSFAPCLIMILIVIRIYLIAKSHRGRPAKGSREGESKQPRVVRGASAK
 ISTLSHQASGEANGHTKPNKGKEGETEDPSPTLPALPHAQGGPKGEGYCG
 VSPREAEDEEEDPVLPAAPASCPPLQOQSGSVLATLRGQVLLGRGVTSQGO
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BASE COUNT 185 a 394 c 346 g 237 t

Query Match 100.0%; Score 21; DB 4; Length 1162;
 Best Local Similarity 100.0%; Pred. No. 18;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 7 AF337538 1167 bp DNA linear MM 22-MAY-2001
 LOCUS AF337538
 DEFINITION Hipposideros commersoni alpha adrenergic receptor 2B (aar2B) gene,
 ACCESSION AF337538
 VERSION AF337538.1 GI:14164927
 KEYWORDS
 SOURCE Hipposideros commersoni (Commerson's roundleaf bat)
 ORGANISM Hipposideros commersoni
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Chiroptera; Microchiroptera; Rhinolophidae;
 Hipposiderinae; Hipposideros.
 1 (bases 1 to 1167)
 Springer, M.S., Teeling, E.C., Madsen, O., Stanhope, M.J. and de
 Jong, M.W.
 Integrated fossil and molecular data reconstruct bat echolocation
 Proc. Natl. Acad. Sci. U.S.A. 98 (11), 6241-6246 (2001)
 11353869
 2 (bases 1 to 1167)
 Springer, M.S., Teeling, E.C., Madsen, O., Stanhope, M.J. and de
 Jong, M.W.
 Direct Submission
 Submitted (17-JAN-2001) Department of Biology, University of
 California, 1354 Speith, Riverside, CA 92521, USA
 Location/Qualifiers
 1. 1167
 /organism="Hipposideros commersoni"
 /mol_type="genomic DNA"
 /db_xref="taxon:110941"
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 LASSIGSFAPCLIMILIVIRIYLIAKSHRGRPAKGSREGESKQPRVVRGASAK
 ISTLSHQASGEANGHTKPNKGKEGETEDPSPTLPALPHAQGGPKGEGYCG
 VSPREAEDEEEDPVLPAAPASCPPLQOQSGSVLATLRGQVLLGRGVTSQGO
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BASE COUNT 191 a 396 c 344 g 235 t 1 others

ORIGIN
 Query Match 100.0%; Score 21; DB 4; Length 1162;
 Best Local Similarity 100.0%; Pred. No. 18;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 8 MAL419805 1167 bp DNA linear MM 08-FEB-2002
 LOCUS MAL419805
 DEFINITION Nyctimene albigaster partial adra2b gene for alpha 2B adrenergic
 receptor.
 ACCESSION AU419805
 VERSION AU419805.1 GI:18643971
 KEYWORDS adra2b gene; alpha 2B adrenergic receptor.
 SOURCE Nyctimene albigaster (common tube-nosed fruit bat)
 ORGANISM Nyctimene albigaster
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Chiroptera; Megachiroptera; Pteropodidae;
 Pteropodinae; Nyctimene.
 1
 Teeling, E.C., Madsen, O., Van den Bussche, R.A., de Jong, M.W.,
 Stanhope, M.J. and Springer, M.S.
 Microbat paraphyly and the convergent evolution of a key innovation
 in Old World rhinolophoid microbats
 Proc. Natl. Acad. Sci. U.S.A. 99 (3), 1431-1436 (2002)
 21819367
 11805285
 2 (bases 1 to 1167)
 Madsen, O.
 Direct Submission
 Submitted (12-NOV-2001) Madsen O., 161 Biochemistry, University of
 Nijmegen, P.O. Box 9101 6500 HB Nijmegen, NETHERLANDS
 Location/Qualifiers
 1. 1167
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 /mol_type="genomic DNA"
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 /db_xref="GI:18643972"
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BASE COUNT 192 a 378 c 348 g 249 t

ORIGIN
 Query Match 100.0%; Score 21; DB 4; Length 1167;
 Best Local Similarity 100.0%; Pred. No. 18;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 9 RCRA19806 1167 bp DNA linear MM 08-FEB-2002
 LOCUS RCRA19806
 DEFINITION Rhinolophus creaghi partial adra2b gene for alpha 2B adrenergic
 receptor.
 ACCESSION RCRA19806
 VERSION RCRA19806.1 GI:18643971
 KEYWORDS adra2b gene; alpha 2B adrenergic receptor.
 SOURCE Rhinolophus creaghi (common tube-nosed fruit bat)
 ORGANISM Rhinolophus creaghi
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Chiroptera; Megachiroptera; Pteropodidae;
 Pteropodinae; Nyctimene.
 1
 Teeling, E.C., Madsen, O., Van den Bussche, R.A., de Jong, M.W.,
 Stanhope, M.J. and Springer, M.S.
 Microbat paraphyly and the convergent evolution of a key innovation
 in Old World rhinolophoid microbats
 Proc. Natl. Acad. Sci. U.S.A. 99 (3), 1431-1436 (2002)
 21819367
 11805285
 2 (bases 1 to 1167)
 Madsen, O.
 Direct Submission
 Submitted (12-NOV-2001) Madsen O., 161 Biochemistry, University of
 Nijmegen, P.O. Box 9101 6500 HB Nijmegen, NETHERLANDS
 Location/Qualifiers
 1. 1167
 /organism="Nyctimene albigaster"
 /mol_type="genomic DNA"
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 ASCLATSGEASRSKPTKEXGGETEDPSPTLPALPHAQGGPKGEGYCG
 EVGEBYGEDEEEDPVLPAAPASCPPLQOQSGSVLATLRGQVLLGRGVTSQGO
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BASE COUNT 191 a 396 c 344 g 235 t 1 others

ACCESSION	J0419806
VERSION	AJ419806.1 GI:18643973
KEYWORDS	adrazb gene; alpha 2B adrenergic receptor.
SOURCE	Rhinolophus creaghi
ORGANISM	Rhinolophus creaghi Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Chiroptera; Microchiroptera; Rhinolophidae; Rhinolophinae; Rhinolophus.
REFERENCE	1 Teeling,E.C., Madsen,O., Van den Bussche,R.A., de Jong,W.W., Asthoe,M.U. and Springer,M.S. Microbat paraphyly and the convergent evolution of a key innovation in Old world rhinolophid microbats Proc. Natl. Acad. Sci. U.S.A. 99 (3), 1431-1436 (2002)
JOURNAL	21819367
PUBMED	11805285
REFERENCE	2 (bases 1 to 1167) Madsen,O. Direct Submission Submitted (12-NOV-2001) Madsen O., 161 Biochemistry, University of Nijmegen, P.O. Box 9101, 6500 HB Nijmegen, NETHERLANDS
AUTHORS	Madsen,O.
TITLE	Location/Qualifiers
JOURNAL	1..1167
FEATURES	/organism="Rhinolophus creaghi" /mol_type="genomic DNA" /db_xref="taxon:178895"
source	1..1167 /gene="adrazb" /db_xref="GI:18643974"
gene	<1..>1167 /gene="adrazb" /codon_start=1 /product="alpha 2B adrenergic receptor" /protein_id="CAD11973.1"
CDS	/db_xref="GI:18643974"
	/translation="RAIATAVTFLFTFGNAVTIVLTSRSRAPONPLVSLAA DIVATILIPPSLANELGTYFRRTWCETVLADVLPTSSIVHLCHISIDRYWAS RALYNSKTRTPRIKCIVLTIVWLIAVAISLEPIVKDPPQPGRPQCKLNQAWYT LASTIASFAFAPCLIMVLYNLAIYLIAKSHRGPRACKDKSPCARVASAK LSTLASHEAASGEENHESKPVNGKEGTPEPSCIPTLPPIVMALPHAGOPTGVCGGGAAG ASPEDAEDEEDCEPOVLAVSPASCSPLQOPQSRLVATRGVTLGRGKAAG GGWRRAOALTREKRFITVALVAVGLCMFPFFFSYGALICPKVPHGLE"
BASE COUNT	195 a 391 c 344 g 235 t 2 others
ORIGIN	
Query Match	100.0%; Score 21; DB 4; Length 1167;
Best Local Similarity	100.0%; Pred. No. 18;
Matches	21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY	1 GCTCATCATCCCTTTCGCCT 21
Db	150 GCTCATCATCCCTTTCGCCT 170
RESULT 10	
PV1251176	
LOCUS	PV1251176 1168 bp DNA linear MAM 01-JUN-2001
DEFINITION	Phoca vitulina partial aar2B gene for alpha adrenergic receptor 2B.
ACCESSION	AJ251176
VERSION	AJ251176.1 GI:11322419
KEYWORDS	aar2B gene; alpha adrenergic receptor 2B.
SOURCE	Phoca vitulina (harbor seal)
ORGANISM	Phoca vitulina Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Carnivora; Plimipedia; Phocidae; Phoca.
REFERENCE	1 Madsen,O., Scally,W., Douady,C.J., Kao,D.Y., DeBruy,R.W., Adkins,R., Armstrong,H.M., Stanhope,W.J., de Jong,W.W. and Springer,M.S. Parallel adaptive radiations in two major clades of placental mammals Nature 409 (6820), 610-614 (2001)
AUTHORS	Madsen,O., Scally,W., Douady,C.J., Kao,D.Y., DeBruy,R.W., Adkins,R., Armstrong,H.M., Stanhope,W.J., de Jong,W.W. and Springer,M.S.
TITLE	Parallel adaptive radiations in two major clades of placental mammals
JOURNAL	Nature 409 (6820), 610-614 (2001)
MEDLINE	21082081
PUBMED	11214318

REFERENCE	AUTHORS	TITLE	JOURNAL
2 (bases 1 to 1168)	Madsen O.	Direct Submission	
		Submitted (18-NOV-1999)	
		University of Nijmegen, P.O. box 9101, 6500 HB Nijmegen, NETHERLANDS	
FEATURES	source	location/Qualifiers	
	gene	1. .1168	
		/organism="phoca vitulina"	
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BASE COUNT	189 a	398 c	351 g
ORIGIN	1	230 t	
Query Match	100.0%;	Score 21;	DB 4; Length 1168;
Best Local Similarity	100.0%;	Pred. No. 18;	
Matches	21;	Conservative 0;	Mismatches 0; Indels 0; Gaps 0;
Oy	1	GCTCATCATCCCTTCCTGCT 21	
Db	151	GCTCATCATCCCTTCCTGCT 171	
RESULT 11			
LOCUS	AF337543	1170 bp	DNA linear MAM 22-MAY-2001
DEFINITION	Taphozous sp. alpha adrenergic receptor 2B (aar2B) gene, partial		
ACCESSION	AF337543		
VERSION	AF337543.1		
KEYWORDS	GI:14164937		
SOURCE	Taphozous sp.		
ORGANISM	Taphozous sp.		
	Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Chiroptera; Microchiroptera; Emballonuridae; Taphozous.		
REFERENCE	1 (bases 1 to 1170)		
AUTHORS	Springer,M.S., Teeling,E.C., Madsen,O., Stanhope,M.J. and de Jong,M.W.		
	Integrated fossil and molecular data reconstruct bat echolocation Proc. Natl. Acad. Sci. U.S.A. 98 (11), 6241-6246 (2001)		
TITLE	2 (bases 1 to 1170)		
JOURNAL	Springer,M.S., Teeling,E.C., Madsen,O., Stanhope,M.J. and de Jong,M.W.		
MEDLINE	Submitted (17-JAN-2001)		
PUBMED	Department of Biology, University of California, 1354 Speich, Riverside, CA 92521, USA		
REFERENCE	Location/Qualifiers		
AUTHORS	1. .1170		
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FEATURES			
source			
	gene		
	mRNA		


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RESULT 14
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LOCUS          Cynocephalus variegatus partial aar2b gene for alpha adrenergic
DEFINITION     receptor 2B.
ACCESSION      AJ251182
VERSION        aar2b gene; alpha adrenergic receptor 2B.
KEYWORDS       Cynocephalus variegatus (Malayan flying lemur)
SOURCE         Cynocephalus variegatus
ORGANISM       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                Mammalia; Eutheria; Dermoptera; Cynocephalidae; Cynocephalus.
REFERENCE      1
AUTHORS        Madgen, O., Scally, M., Donady, C.J., Kao, D.J., Debry, R.W., Adkins, R.,
                Amrine, H.W., Stanhope, M.J., de Jong, W.W. and Springer, M.S.
TITLE          Parallel adaptive radiations in two major clades of placental
                mammals
JOURNAL        Nature 409 (6820), 610-614 (2001)
MEDLINE        21082081
PUBMED         11214318
REFERENCE      2 (bases 1 to 1171)
AUTHORS        Madgen, O.
TITLE          Direct Submission
                Submitted (18-NOV-1999) Madgen O., Department of Biochemistry,
                University of Nijmegen, P.O. box 9101, 6500 HB Nijmegen,
                NETHERLANDS
FEATURES       source
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                1..1171
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                DLVALIIPSLANELLGYWFFRWCEVTLADVLFTSTSYHLCAISLDRYAVAS
                RALBNKRTPRIRKICILITVWLIAAVISLPLIYKGQGPQIPGRPOCKLNQENWYILAS
                SIGSFAPCLIMILVLRILYIAKSRHGRGAKGPKVVSQKBPVPGGTVPAGAKV
                AKLPAQASPLASAGANGSKPTGKEGSEISDPGTOTLPSWTALPNSGGQKGEV
                CGASRGEAEEREEBCEBPQAVSVASISCPLOQPGSRVATLRGHVTLGRGVG
                GGQWRRRAQLSRERKFTFLAVVIGAFVLCWPFPPFSYSLGATCPQRCVPHGLF"
BASE COUNT    173 a      388 c      369 g      241 t
ORIGIN
Query Match   100.0%; Score 21; DB 9; Length 1171;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY            1 GGTCAATCATCCTTCTCGCT 21
                |||||
                151 GGTCAATCATCCTTCTCGCT 171
Db

```

```

AUTHORS        Huchon, D., Madgen, O., Sibbald, M.J., Ament, K., Stanhope, M.J.,
                Catzefflis, F., de Jong, W.W. and Douzery, E.J.
TITLE          Rodent phylogeny and a timescale for the evolution of Glires:
                evidence from an extensive taxon sampling using three nuclear genes
JOURNAL        Mol. Biol. Evol. 19 (7), 1053-1065 (2002)
MEDLINE        22077630
PUBMED         12082125
REFERENCE      2 (bases 1 to 1172)
AUTHORS        Douzery, E.J.P.
TITLE          Direct Submission
                Submitted (04-JUN-2002) Douzery, E.J.P., Institut des Sciences de
                l'Evolution, Lab. Paleont., Paleobio., Phylogenie, Universite
                Montpellier II, Pl. E. Bataillon, 34 095 Montpellier Cedex 5,
                FRANCE
FEATURES       source
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                /product="alpha 2B adrenergic receptor"
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                /db_xref="GI:21655548"
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                EYNSKRTPRIRKICILITVWLIAAVISLPLIYKGQGPQIPGRPOCKLNQENWYILAS
                SIGSFAPCLIMILVLRILYIAKSRHGRGAKGPKVVSQKBPVPGGTVPAGAKV
                PTIASPLSPGANGHPKPTGKEGSEITLSEGTALPASWTALPEADOGKTSFCGA
                SPEERGEEREEBCEBCEBPQAVSVASISCPLOQPGSRVATLRGHVTLGRGVG
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BASE COUNT    202 a      386 c      348 g      236 t
ORIGIN
Query Match   100.0%; Score 21; DB 10; Length 1172;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY            1 GGTCAATCATCCTTCTCGCT 21
                |||||
                141 GGTCAATCATCCTTCTCGCT 161
Db

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 Job time : 618.146 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: February 12, 2004, 01:53:19 ; Search time 110.378 Seconds
(without alignments)
513.582 Million cell updates/sec

Title: US-09-692-077D-13

Perfect score: 21

Sequence: 1 gctcatcacccttcctcgct 21

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 2552756 seqs, 1349719017 residues

Total number of hits satisfying chosen parameters: 5105512

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	21	100.0	21	AA199907	Human alpha-2BAR g
2	21	100.0	1344	AA199907	Human alpha-2BAR g
3	21	100.0	1344	AA199906	Human alpha-2BAR t
4	21	100.0	1344	AA199906	Human alpha-2BAR t
5	21	100.0	1353	AA199905	Human alpha-2BAR t
6	21	100.0	1353	AA199905	Human alpha-2BAR t
7	21	100.0	1353	AA199905	Human alpha-2BAR t
8	21	100.0	2072	ACAS6583	Human alpha-2B-adr

9	21	100.0	3274	AB242624	Human alpha 2b-adr
10	21	100.0	6904	ABL32075	Human immune syste
11	21	100.0	6904	ABD28365	Human chemically t
12	19.4	92.4	1350	AA199917	Human alpha-2BAR e
13	19.4	92.4	1350	AA199917	Human alpha-2BAR e
14	19.4	92.4	1733	ABQ47500	Human alpha-2BAR v
15	19.4	92.4	1733	ABQ47501	Oligonucleotide fo
16	19.4	92.4	1733	ABQ47501	Oligonucleotide fo
17	19.4	92.4	2064	AAQ14151	Human alpha 2 beta
18	19.4	92.4	2064	AAQ14151	Human alpha-2b adr
19	19.4	92.4	3604	ACA55582	Human alpha-2b adr
20	19.4	92.4	3604	ACA55582	Human alpha-2b adr
21	19.4	92.4	3653	AB242623	Human alpha 2a-adr
22	19.4	92.4	7353	ABL32073	Human immune syste
23	19.4	92.4	7353	ABD28363	Human chemically t
24	18.4	87.6	297	ABX83493	Corn ear-derived p
25	17.8	84.8	3840	ABL18139	Drosophila melanog
26	17.8	84.8	7720	ABL18138	Drosophila melanog
27	16.8	80.0	261	AA199918	Human alpha 2a-adr
28	16.8	80.0	376	ABV13690	Human prostate exp
29	16.8	80.0	401	ABV04521	Human prostate exp
30	16.8	80.0	401	ABV34803	Human prostate exp
31	16.8	80.0	967	AA176276	Human prostate exp
32	16.8	80.0	7327	ABL08624	Maize glutathione-
33	16.8	80.0	7933	ABL08720	Drosophila melanog
34	16.4	78.1	954	AA542448	Drosophila melanog
35	16.4	78.1	954	ABN89118	Human CDNA encodin
36	16.4	78.1	954	ABN89119	Human GPCR4a nucle
37	16.4	78.1	954	ABK37734	Human GPCR4a nucle
38	16.4	78.1	958	ABT05663	DNA encoding G-con
39	16.4	78.1	958	ABQ08380	GPCR 12 protein en
40	16.4	78.1	958	ABN89127	Human GPCR8a nucle
41	16.4	78.1	958	ABN89128	Human GPCR8a nucle
42	16.4	78.1	1017	AA542422	Human CDNA encodin
43	16.4	78.1	1017	ABK37708	Human GPCR polynuc
44	16.4	78.1	1049	AAH32040	DNA encoding G-con
45	16.4	78.1	1408	ABX17873	Human olfactory re

ALIGNMENTS

AA199907	AA199907 standard; DNA; 21 BP.
AA199907	AA199907; (first entry)
AA199907	18-FEB-2002 (first entry)
AA199907	Human alpha-2BAR genotyping PCR primer SEQ ID NO 13.
AA199907	Human; genotyping; alpha-2B; alpha-2A; alpha-2C; adrenergic receptor;
AA199907	polymorphic site; allelic variant; cardiovascular disease;
AA199907	central nervous system disease; adenylyl cyclase; MAP kinase activity;
AA199907	phosphorylation; inositol phosphate; alpha-2BAR; PCR primer; ss.
AA199907	Homo sapiens.
AA199907	WO200179561-A2.
AA199907	25-OCT-2001.
AA199907	17-APR-2001; 2001WO-US12575.
AA199907	17-APR-2000; 2000US-0551744.
AA199907	10-AUG-2000; 2000US-0636259.
AA199907	19-OCT-2000; 2000US-0692077.
AA199907	(LIGG/) LIGGETT S B.
AA199907	(SMAL/) SMALL K M.
AA199907	Liggett SB, Small KM;

XX DR WPI, 2001-611728/70.
 XX
 XX Genotyping an alpha-2B, 2A, or 2C adrenergic receptor gene useful for
 PT determining whether an individual is at increased risk of developing a
 PT disease associated with the corresponding receptor comprises detecting
 PT a polymorphic site -
 XX
 XX Claim 10; Page 112; 163pp; English.

XX The invention relates to genotyping an alpha-2B, 2A, or 2C adrenergic
 CC receptor gene (I)-(III) by detecting a polymorphic site, comprising:
 CC (a) obtaining a sample having a polynucleotide encoding an alpha-2B,
 CC alpha2A or alpha2C or fragment or complement of; and
 CC (b) detecting a polymorphic site comprising nucleotide positions 901-909
 CC of (I), a site comprising cytosine or guanine at position 753 of (IIIV)
 CC or a site comprising (A) (999ggcgggcg) or (B) (99ggcgggcg) at
 CC positions 961-972 of (III). The method may be used for genotyping an
 CC alpha2B, alpha2A or alpha2C receptor gene and further used to determine
 CC whether an individual is at increased risk of developing a disease
 CC associated with alpha2B, alpha2A or alpha2, comprising detecting a
 CC polymorphic site which correlate to disease selected from cardiovascular
 CC disease, central nervous system disease and combinations of these. In
 CC addition, the technique may be used to predict an individual's response
 CC to an alpha2B, alpha2A, or alpha2C agonist (e.g. epinephrine,
 CC norepinephrine, clonidine, oxymetazoline, guanabenz, UK14304, BHT933 and
 CC combinations of these) or antagonist (e.g. yohimbine, prazosin, ARC 239,
 CC rauwolfazine, idazoxan, tolazoline, phenolamine and combinations of
 CC these) by detecting the polymorphic site and correlating the site to a
 CC predetermined response (where the response is correlated to adenylyl
 CC cyclase, MAP kinase activity, phosphorylation or inositol phosphate
 CC levels). The present sequence is that of a human alpha-2BAR PCR primer,
 CC useful for the genotyping methods of the invention.

XX SQ Sequence 21 BP; 2 A; 9 C; 2 G; 8 T; 0 other;

Query Match 100.0%; Score 21; DB 23; Length 21;
 Best Local Similarity 100.0%; Pred. No. 2;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCATCATCCCTTTCGCT 21
 |||||
 DB 1 GCTCATCATCCCTTTCGCT 21

RESULT 2

ID AAD04761 standard; DNA; 1344 BP.

XX AAD04761;

DT 04-JUL-2001 (first entry)

DE Human alpha2B-adrenoceptor (alpha2B-AR) variant gene.

XX Human; cardiac; gene therapy; alpha2B-adrenoceptor; alpha2B-AR;
 KW glutamic acid repeat; intracellular loop; chromosome 2; catecholamine;
 KW norepinephrine; epinephrine; therapy; vascular contraction; variant;
 KW coronary artery; coronary heart disease; CHD; chronic angina pectoris;
 KW acute myocardial infarction; AMI; Primmetal's variant; ds.

XX Homo sapiens.

OS Location/Qualifiers

XX Key 1..1344

XX CDS

FT /tag= a
 FT /product= "Human alpha2B-adrenoceptor (alpha2B-AR)
 FT variant protein"

XX WO200129082-A1.

XX 26-APR-2001.

PF 20-OCT-2000; 2000WO-FI00913.

XX 22-OCT-1999; 99US-0422985.

XX (JUVA-) JUVANTIA PHARMA LTD OY.

PI Snapir A, Heinoonen P, Alhopuro P, Karvonen M, Koulu M, Pesonen U;
 PI Scheinin M, Salonen JT, Tuomala T, Lakka TA, Nyyssönen K;
 PI Salonen R, Kauphanen J, Valkonen V;

XX WPI; 2001-300318/31.

XX P-PSDB; AAE00989.

PT New DNA molecule encoding variant specific adrenoceptor protein with
 PT deletion of specific amino acids located in the third intracellular
 PT loop of the polypeptide, for treating vascular contraction of coronary
 PT arteries -
 XX
 XX Claim 3; Page 24-26; 37pp; English.

XX The present sequence is a gene encoding human alpha2B-adrenoceptor
 CC (alpha2B-AR) variant protein. Alpha2B-AR has a glutamic acid repeat
 CC element (amino acids 298-309) of 12 glutamates, in an acidic stretch of
 CC 18 amino acids (amino acids 294-311), located in the third intracellular
 CC loop of the receptor polypeptide. The variant is obtained by deletion of
 CC three glutamates from the Glu repeat (amino acids 307-309). Alpha2B-AR
 CC gene is located on chromosome 2. Alpha2-AR mediate many of the
 CC physiological effects of the catecholamines, norepinephrine and
 CC epinephrine. An antagonist of alpha2B-adrenoceptor is useful for treating
 CC a mammal suffering from vascular contraction of coronary arteries and a
 CC disease involving vascular contraction of coronary arteries which is
 CC clinically expressed as coronary heart disease (CHD), unstable chronic
 CC angina pectoris which is clinically expressed as Primmetal's variant
 CC form or acute myocardial infarction (AMI). Alpha2B-AR gene is used in
 CC gene therapy.

XX SQ Sequence 1344 BP; 219 A; 459 C; 400 G; 266 T; 0 other;

Query Match 100.0%; Score 21; DB 22; Length 1344;
 Best Local Similarity 100.0%; Pred. No. 3.2;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCATCATCCCTTTCGCT 21
 |||||
 DB 189 GCTCATCATCCCTTTCGCT 209

RESULT 3

ID AAI99906 standard; DNA; 1344 BP.

XX AAI99906;

DT 18-FEB-2002 (first entry)

DE Human alpha-2BAR third intracellular loop variant encoding DNA.

XX Human; genotyping; alpha-2B; alpha-2A; alpha-2C; adrenergic receptor;
 KW polymorphic site; allelic variant; cardiovascular disease;
 KW central nervous system disease; adenylyl cyclase; MAP kinase activity;
 KW phosphorylation; inositol phosphate; alpha-2BAR; chromosome 2; ds.

XX Homo sapiens.

OS Location/Qualifiers

XX Key 1..1344

XX CDS

FT /tag= a
 FT /product= "alpha-2BAR"
 FT /note= "sequence is deleted for a 9 nucleotide
 FT polymorphic site found at nucleotides 901-909
 FT of the wildtype alpha-2BAR protein (AAI99905)"
 XX

XX WO200179561-A2.

XX 25-OCT-2001.
 PD 17-APR-2001; 2001MO-US12575.
 XX PF
 XX 17-APR-2001; 2000US-0551744.
 XX PR 10-AUG-2000; 2000US-0636259.
 PR 19-OCT-2000; 2000US-0692077.
 XX
 PA (LIGGETT) LIGGETT S B.
 PA (SMALL) SMALL K M.
 XX
 PI Liggett SB, Small KM;
 XX
 XX WPI: 2001-611728/70.
 DR P-PSDB; AAM52118.
 XX
 XX Genotyping an alpha-2B, 2A, or 2C adrenergic receptor gene useful for
 PT determining whether an individual is at increased risk of developing a
 PT disease associated with the corresponding receptor comprises detecting
 PT a polymorphic site -
 XX
 PS Claim 5; Page 144-145; 163pp; English.
 XX
 XX The invention relates to genotyping an alpha-2B, 2A, or 2C adrenergic
 CC receptor gene (I)-(III) by detecting a polymorphic site, comprising:
 CC (a) obtaining a sample having a polynucleotide encoding an alpha-2B,
 CC alpha2A or alpha2C or fragment or complement of; and
 CC (b) detecting a polymorphic site comprising nucleotide positions 901-909
 CC of (I), a site comprising cytosine or guanine at position 753 of (IIV)
 CC or a site comprising (A) (999GCG99GCG) or (B) (999GCG9GCG) at
 CC positions 961-972 of (III). The method may be used for genotyping an
 CC alpha2B, alpha2A or alpha2C receptor gene and further used to determine
 CC whether an individual is at increased risk of developing a disease
 CC associated with alpha2B, alpha2A or alpha2C, comprising detecting a
 CC polymorphic site which correlate to disease selected from cardiovascular
 CC disease, central nervous system disease and combinations of these. In
 CC addition, the technique may be used to predict an individual's response
 CC to an alpha2B, alpha2A, or alpha2C agonist (e.g. epinephrine,
 CC norepinephrine, clonidine, oxymetazoline, guanabenz, UK14304, BHT933 and
 CC combinations of these) or antagonist (e.g. yohimbine, prazosin, ARC 239,
 CC rauwolficine, idazoxan, tolazoline, phenolamine and combinations of
 CC these) by detecting the polymorphic site and correlating the site to a
 CC predetermined response (where the response is correlated to adenylyl
 CC cyclase, MAP kinase activity, phosphorylation or inositol phosphate
 CC levels). The present sequence is that of the third intracellular loop of
 CC the human alpha-2BAR variant, the sequence is deleted for a 9 nucleotide
 CC polymorphic site found at nucleotides 901-909 of the wildtype gene
 CC (AA199905).
 CC
 XX
 SO Sequence 1344 BP; 220 A; 458 C; 400 G; 266 T; 0 other;

Query Match 100.0%; Score 21; DB 23; Length 1344;
 Best Local Similarity 100.0%; Pred. No. 3.2;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCATCATCCTTTCTCGCT 21
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 DB 189 GCTCATCATCCTTTCTCGCT 209

RESULT 4
 AAD44388
 ID AAD44388 standard; DNA; 1344 BP.
 XX
 AC AAD44388;
 XX
 XX 13-DEC-2002 (first entry)
 DT
 XX
 DE Human alpha-2B-adrenoceptor variant DNA.
 XX
 XX Human; hypertension; alpha-2B-adrenoceptor; AR; antihypertensive;
 KW hypertension; hypotensive; variant; gene; ds.

XX Homo sapiens.
 OS Synthetic.
 OS
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 XX Key Location/Qualifiers
 FT CDS 1..1344
 FT /tag= a
 FT /product= "Human alpha-2B-adrenoceptor variant
 FT protein"
 XX
 PN WO20026617-A1.
 XX
 PD 29-AUG-2002.
 XX
 XX 13-FEB-2002; 2002MO-FI00113.
 PF
 XX 20-FEB-2001; 2001FI-0000323.
 PR
 XX (JURI-) JURILAB LTD OY.
 PA
 XX Salonen J;
 PI
 XX WPI: 2002-667063/71.
 DR P-PSDB; AAE26633.
 DR
 XX
 XX Detecting a risk of hypertension and targeting treatment in a subject
 PT by determining the pattern of alleles encoding a variant
 PT alpha-2-adrenoceptor -
 PT
 XX
 PS Disclosure; Page 24-26; 35pp; English.
 XX
 XX The invention relates to a method for detecting a risk of hypertension
 CC by determining the pattern of alleles encoding a variant alpha-2B-
 CC adrenoceptor (AR) protein. The methods and compositions of the invention
 CC are useful for detecting risks and targeting treatment for hypertension.
 CC The kit is also useful for selecting for clinical drug trials testing
 CC the antihypertensive effect of compounds. The present sequence is human
 CC alpha-2B-adrenoceptor variant DNA.
 CC
 XX
 SO Sequence 1344 BP; 219 A; 459 C; 400 G; 266 T; 0 other;

Query Match 100.0%; Score 21; DB 24; Length 1344;
 Best Local Similarity 100.0%; Pred. No. 3.2;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCATCATCCTTTCTCGCT 21
 |||||
 DB 189 GCTCATCATCCTTTCTCGCT 209

RESULT 5
 AAD04762
 ID AAD04762 standard; DNA; 1353 BP.
 XX
 AC AAD04762;
 XX
 XX 04-JUL-2001 (first entry)
 DT
 XX
 DE Human alpha2B-adrenoceptor (alpha2B-AR) gene.
 XX
 XX Human; cardiac; gene therapy; alpha2B-adrenoceptor; alpha2B-AR;
 KW glutamic acid repeat; intracellular loop; chromosome 2; catecholamine;
 KW norepinephrine; epinephrine; therapy; vascular contraction;
 KW coronary artery; coronary heart disease; CHD; chronic angina pectoris;
 KW acute myocardial infarction; AMI; Prinzmetal's variant; ds.
 XX
 OS Homo sapiens.
 OS
 XX
 XX Key Location/Qualifiers
 FT CDS 1..1353
 FT /tag= a
 FT /product= "Human alpha2B-adrenoceptor (alpha2B-AR)
 FT protein"

XX PN WO200129082-A1.
XX XX 26-APR-2001.
XX PD 20-OCT-2000; 2000WO-FI00913.
XX PF 22-OCT-1999; 99US-0422985.
XX PR (JUVANTIA PHARMA LTD OY.
XX PA Snadir A, Heinonen P, Alhopuro P, Karvonen M, Koulu M, Pesonen U,
XX PI Scheinin M, Salonen JT, Tuomainen T, Lakka TA, Myysoenen K;
XX PI Salonen R, Kaunen U, Valkonen V;
XX XX WPI: 2001-300318/31.
XX DR P-PSDB; AAB00990.
XX XX
XX PT New DNA molecule encoding variant specific adrenoceptor protein with
XX PT deletion of specific amino acids located in the third intracellular
XX PT loop of the polypeptide, for treating vascular contraction of coronary
XX PT arteries -
XX PS Disclosure; Page 27-29; 37pp; English.
XX XX
XX CC The present sequence is a gene encoding human alpha2B-adrenoceptor
XX CC (alpha2B-AR) protein. Alpha2B-AR has a glutamic acid repeat element
XX CC (amino acids 298-309) of 12 glutamates, in an acidic stretch of 18 amino
XX CC acids (amino acids 294-311), located in the third intracellular loop of
XX CC the receptor polypeptide. Alpha2B-AR gene is located on chromosome 2.
XX CC Alpha2B-AR mediate many of the physiological effects of the
XX CC catecholamines, norepinephrine and epinephrine. An antagonist of
XX CC vascular contraction of coronary arteries and a disease involving
XX CC as coronary heart disease (CHD), unstable chronic angina pectoris which is
XX CC clinically expressed as Prinzmetal's variant form or acute myocardial
XX CC infarction (AMI). Alpha2B-AR gene is used in gene therapy.
XX XX
XX SQ Sequence 1353 BP; 223 A; 459 G; 405 G; 266 T; 0 other;
XX
XX Query Match 100.0%; Score 21; DB 22; Length 1353;
XX Best Local Similarity 100.0%; Pred. No. 3.2;
XX Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX OY 1 GGTCTCATCCCTTCTCGCT 21
XX DB 189 GCTCATCATCCCTTCTCGCT 209
XX
XX RESULT 6
XX AA199905
XX ID AA199905 standard; DNA, 1353 BP.
XX AC AA199905;
XX XX
XX DT 18-FEB-2002 (first entry)
XX XX
XX DE Human alpha-2BAR third intracellular loop encoding DNA.
XX XX
XX KM Human; genotyping; alpha-2B; alpha-2A; alpha-2C; adrenergic receptor;
XX KM polymorphic site; allelic variant; cardiovascular disease;
XX KM central nervous system disease; adenylyl cyclase; MAP kinase activity;
XX KM phosphorylation; inositol phosphate; alpha-2BAR;
XX KM GenBank Accession AF009500; chromosome 2; db.
XX XX
XX OS Homo sapiens.
XX XX
XX FH Key
XX FT CDS
XX FT 1..1353
XX FT /tag= a
XX FT /product= "alpha-2BAR"
XX FT /note= "sequence includes a 9 nucleotide polymorphic site

FT FT at nucleotides 901-909 absent in the alpha-2BAR
XX XX variant (AA199906)"
XX PN WO200179561-A2.
XX XX 25-OCT-2001.
XX PD 17-APR-2001; 2001WO-US12575.
XX PF 17-APR-2000; 2000US-0551744.
XX PR 10-AUG-2000; 2000US-0636259.
XX PR 19-OCT-2000; 2000US-0692077.
XX XX (LIGGETT S B.
XX PA (SMALL) SMALL K M.
XX PI Liggett SB, Small KM;
XX XX WPI: 2001-611728/70.
XX DR P-PSDB; AAM52117.
XX XX
XX PT Genotyping an alpha-2B, 2A, or 2C adrenergic receptor gene useful for
XX PT determining whether an individual is at increased risk of developing a
XX PT disease associated with the corresponding receptor comprises detecting a
XX PT polymorphic site -
XX PS Claim 4; Page 144; 163pp; English.
XX XX
XX CC The invention relates to genotyping an alpha-2B, 2A, or 2C adrenergic
XX CC receptor gene (I)-(III) by detecting a polymorphic site, comprising:
XX CC (a) obtaining a sample having a polynucleotide encoding an alpha-2B,
XX CC alpha2A or alpha2C or fragment or complement of; and
XX CC (b) detecting a polymorphic site comprising nucleotide positions 901-909
XX CC or a site comprising (A) (ggggcgggcg) or (B) (ggggcggtgag) at
XX CC positions 961-972 of (III). The method may be used for genotyping an
XX CC alpha2B, alpha2A or alpha2C receptor gene and further used to determine
XX CC whether an individual is at increased risk of developing a disease
XX CC associated with alpha2B, alpha2A or alpha2C, comprising detecting a
XX CC polymorphic site which correlate to disease selected from cardiovascular
XX CC disease, central nervous system disease and combinations of these. In
XX CC addition, the technique may be used to predict an individual's response
XX CC to an alpha2B, alpha2A, or alpha2C agonist (e.g. epinephrine,
XX CC norepinephrine, clonidine, oxymetazoline, guanadenz, UK14304, BHT933 and
XX CC combinations of these) or antagonist (e.g. yohimbine, prazosin, ARC 239,
XX CC rauwolfscine, idazoxan, tolazoline, phenolamine and combinations of
XX CC these) by detecting the polymorphic site and correlating the site to a
XX CC predetermined response (where the response is correlated to adenylyl
XX CC cyclase, MAP kinase activity, phosphorylation or inositol phosphate
XX CC levels). The present sequence is that of the third intracellular loop of
XX CC the human alpha-2BAR (GenBank Accession AF009500), the sequence includes
XX CC alpha-2BAR variant (AA199906).
XX XX
XX SQ Sequence 1353 BP; 224 A; 458 G; 405 G; 266 T; 0 other;
XX
XX Query Match 100.0%; Score 21; DB 23; Length 1353;
XX Best Local Similarity 100.0%; Pred. No. 3.2;
XX Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX OY 1 GGTCTCATCCCTTCTCGCT 21
XX DB 189 GCTCATCATCCCTTCTCGCT 209
XX
XX RESULT 7
XX AAD44389
XX ID AAD44389 standard; DNA, 1353 BP.
XX AC AAD44389;
XX XX
XX DT 13-DEC-2002 (first entry)
XX XX

DE Human alpha-2b-adrenoceptor gene.
XX
XX Human; hypertension; alpha-2b-adrenoceptor; AR; antihypertensive;
KW hypertension; hypotensive; gene; ds.
XX
XX Homo sapiens.
OS
XX
XX Key Location/Qualifiers
FH 1..1353
FT CDS /tag= a
FT /product= "Human alpha-2b-adrenoceptor protein"
PT
XX WO200266617-A1.
XX
XX 29-AUG-2002.
XX
XX 13-FEB-2002; 2002WO-FI00113.
XX
XX 20-FEB-2001; 2001FI-0000323.
XX
XX (JURL-) JURILAB LTD OY.
XX
XX Salonen J;
PI
XX MPI; 2002-667063/71.
XX
XX P-PSDB; AAE26634.
DR
XX
XX Detecting a risk of hypertension and targeting treatment in a subject
PT by determining the pattern of alleles encoding a variant
PT alpha-2-adrenoceptor -
XX
XX Disclosure; Page 27-29; 35pp; English.
XX
XX The invention relates to a method for detecting a risk of hypertension
CC by determining the pattern of alleles encoding a variant alpha-2b-
CC adrenoceptor (AR) protein. The methods and compositions of the invention
CC are useful for detecting risks and targeting treatment for hypertension.
CC The kit is also useful for selecting for clinical drug trials testing
CC the antihypertensive effect of compounds. The present sequence is human
CC alpha-2b-adrenoceptor gene.
XX
XX
SQ Sequence 1353 BP; 223 A; 459 C; 405 G; 266 T; 0 other;
Query Match 100.0%; Score 21; DB 24; Length 1353;
Best Local Similarity 100.0%; Pred. No. 3.2;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GCTCATCATCCTTCTCGCT 21
DB 189 GCTCATCATCCTTCTCGCT 209
RESULT 8
ACAS6583
ID ACAS6583 standard; cDNA; 2072 BP.
XX
XX ACAS6583;
AC
XX
XX 06-JUN-2003 (first entry)
DT
XX
XX Human signalling pathway polynucleotide probe SEQ ID NO 1181.
DE
XX
XX Human; probe; ss; array element; Parkinson's disease;
KW signalling pathway population; cancer; adenocarcinoma; leukaemia;
KW immunopathy; AIDS; asthma; neuropathy; Alzheimer's disease; microarray.
XX
XX Homo sapiens.
OS
XX
XX US6500938-B1.
XX
XX 31-DEC-2002.
PD
XX
XX 30-JAN-1998; 98US-0016434.
PF

XX
XX 30-JAN-1998; 98US-0016434.
PR
XX
XX (INCY-) INCYTE GENOMICS INC.
PA
XX
XX Au-Young J, Seilhamer JJ;
PI
XX
XX MPI; 2003-352189/33.
DR
XX
XX Combination of polynucleotide probes, useful as array elements in a
PT microarray for monitoring the expression of a number of target
PT polynucleotides -
XX
XX
XX Claim 1; SEQ ID NO 1181; 65pp; English.
PS
XX
XX The invention relates to a combination which, comprises a number of
CC polynucleotide probes comprising a sequence selected from one of the 1490
CC sequences mentioned in the specification. The combination is useful as an
CC array element in a microarray for monitoring the expression of a number
CC of target polynucleotides. The microarray is particularly useful in the
CC diagnosis and treatment of cancer and immunopathology and neuropathology.
CC The microarray is useful in diagnostics and treatment regimens, drug
CC discovery and development, toxicological and carcinogenicity studies,
CC forensics and pharmacogenomics. The microarray is also useful for
CC monitoring progression of diseases and for developing sophisticated
CC profiles for the effects of currently available therapeutic drugs. The
CC combination is also useful for purifying a subpopulation of mRNAs, cDNAs
CC and genomic fragments and in research and diagnostic applications. The
CC array can detect changes in expression in a large number of genes coding
CC for different signalling pathway populations which can be used to diagnose
CC various diseases including cancer e.g. adenocarcinoma and leukaemia,
CC immunopathies e.g. AIDS and asthma, neuropathies e.g. Alzheimer's disease
CC and Parkinson's disease. The present sequence represents a polynucleotide
CC probe of the invention.
CC Note: The sequence data for this patent did not form part of the printed
CC specification but was obtained in electronic format directly from USPTO
CC at seqdata.uspto.gov/sequence.html?docID=06500938B1.
XX
XX
SQ Sequence 2072 BP; 316 A; 705 C; 660 G; 391 T; 0 other;
Query Match 100.0%; Score 21; DB 25; Length 2072;
Best Local Similarity 100.0%; Pred. No. 3.4;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GCTCATCATCCTTCTCGCT 21
DB 601 GCTCATCATCCTTCTCGCT 621
RESULT 9
ABZ42624
ID ABZ42624 standard; DNA; 3274 BP.
XX
XX ABZ42624;
AC
XX
XX 04-MAR-2003 (first entry)
DT
XX
XX Human alpha 2b-adrenoceptor nucleotide SEQ ID NO:41.
DE
XX
XX G protein-coupled receptor; GPCR; antigenic peptide; gene therapy;
KW G protein-coupled receptor modulator; antibody; immune-related disease;
KW growth-related disease; cell regeneration-related disease; AIDS; cancer;
KW immunological-related cell proliferative disease; autoimmune disease;
KW Alzheimer's disease; atherosclerosis; infection; osteoarthritis; allergy;
KW osteoporosis; cardiomyopathy; inflammation; Crohn's disease; diabetes;
KW gastritis; host disease; Parkinson's disease; multiple sclerosis; pain;
KW psoriasis; anxiety; depression; schizophrenia; dementia; memory loss;
KW mental retardation; epilepsy; asthma; tuberculosis; obesity; nausea;
KW hypertension; hypotension; renal disorder; rheumatoid arthritis; trauma;
KW ulcer; gene; ds.
XX
XX
XX Homo sapiens.
OS

PN WO200261087-A2.
 XX
 PD 08-AUG-2002.
 XX
 PF 19-DEC-2001, 2001WO-US50107.
 XX
 PR 19-DEC-2000, 2000US-257144P.
 XX
 PA (LIFE-) LIFESPAN BIOSCIENCES INC.
 XX
 PI Burner GC, Roush CL, Brown JP,
 XX
 DR WPI; 2003-046718/04.
 XX
 DR P-PSDB; ABP81780.
 XX
 PT New isolated antigenic peptides e.g., for G protein-coupled receptors
 PT (GPCR), useful for diagnosing and designing drugs for treating
 PT conditions in which GPCRs are involved, e.g. AIDS, Alzheimer's disease,
 PT cancer or autoimmune diseases
 XX
 PS Disclosure; Fig 1, 523pp; English.
 XX
 CC The present invention describes antigenic peptides (I) comprising:
 CC (a) any one of 1601 sequences (see ABP82019 to ABP83619) of 12-24 amino
 CC acids. Also described: (1) an assay for the detection of a particular
 CC G protein-coupled receptor (GPCR) or a candidate polypeptide in a sample;
 CC and (2) an isolated antibody having high specificity and high affinity
 CC or avidity for a particular GPCR. (1) can be used as GPCR modulators and
 CC in gene therapy. The antigenic peptides for GPCRs are useful in detecting
 CC an antibody against a particular GPCR, and in the production of detecting the
 CC presence or absence of corresponding GPCRs. The antigenic peptides for
 CC GPCRs and antibodies are also useful for diagnosing and designing drugs for
 CC treating immune-related diseases, growth-related diseases, cell
 CC regeneration-related diseases, immunological-related diseases, cell
 CC diseases, or autoimmune diseases, e.g. AIDS, Alzheimer's disease,
 CC atherosclerosis, bacterial, fungal, protozoan or viral infections,
 CC osteoarthritis, osteoporosis, cancer, catatonia or viral infections,
 CC inflammation, allergies, Crohn's disease, diabetes, graft versus host
 CC disease, Parkinson's disease, multiple sclerosis, pain, psoriasis,
 CC anxiety, depression, schizophrenia, dementia, mental retardation, memory
 CC loss, epilepsy, asthma, tuberculosis, obesity, hypertension, memory
 CC hypotension, renal disorders, rheumatoid arthritis, trauma, ulcers, or
 CC any other disorder in which GPCRs are involved. The antibodies may be
 CC used in immunoassays and immunodiagnosis. ABZ42523 to ABZ42869 encode
 CC GPCR proteins given in ABP81675 to ABP82018, which are used in the
 CC exemplification of the present invention.
 XX
 SQ Sequence 3274 BP; 587 A; 979 C; 967 G; 741 T; 0 other;

Query Match 100.0%; Score 21; DB 25; Length 3274;
 Best Local Similarity 100.0%; Pred. No. 3.6;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GCTCATCATCCCTTCTCGCT 21
 DB 189 GCTCATCATCCCTTCTCGCT 209

RESULT 10
 ABL32075/c
 ID ABL32075 standard; DNA; 6904 BP.
 XX
 AC ABL32075;
 XX
 DT 26-MAR-2002 (first entry)
 XX
 DE Human immune system associated gene SEQ ID NO: 48.
 XX
 KM Human: immune system disease; cytosine methylation; antiasthmatic;
 KM antiarteriosclerotic; antiamebic; cytosine methylation; nootropic;
 KM neuroprotective; anti-HIV; anticonvulsant; ophthalmological;
 KM antirheumatic; antiarthritic; antidiabetic; antipsoriatic;

KM antiinflammatory; cancer; eye disease; arteriosclerosis; anaemia;
 KM acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy;
 KM neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease;
 KM gene; ds.
 OS Homo sapiens.
 XX
 PN WO200200928-A2.
 XX
 PD 03-JAN-2002.
 XX
 PF 02-JUL-2001, 2001WO-EP07537.
 XX
 PR 30-JUN-2000; 2000DE-1032529.
 XX
 PR 01-SEP-2000; 2000DE-1043826.
 XX
 PA (EPIC-) EPIDEMICS AG.
 XX
 PI Olek A, Piepenbrock C, Berlin K;
 XX
 DR WPI; 2002-130909/17.
 XX
 PT Nucleic acid comprising fragment of chemically modified gene, useful
 PT for diagnosis and treatment of diseases associated with abnormal
 PT cytosine methylation
 XX
 PS Claim 1, SEQ ID NO 48; 32pp + Sequence Listing; German.
 XX
 CC The present invention provides a number of human immune system associated
 CC genes which are modified by the methylation of cytosines. The sequences
 CC can be used in the diagnosis and treatment of immune system disorders,
 CC including eye diseases such as retinopathy, neovascular glaucoma and
 CC macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid
 CC leukaemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis,
 CC rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel
 CC diseases. The present sequence is a gene of the invention.
 XX
 SQ Sequence 6904 BP; 1326 A; 314 C; 2030 G; 3233 T; 1 other;

Query Match 100.0%; Score 21; DB 24; Length 6904;
 Best Local Similarity 100.0%; Pred. No. 3.9;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GCTCATCATCCCTTCTCGCT 21
 DB 1716 GCTCATCATCCCTTCTCGCT 1696

RESULT 11
 AAD28365/c
 ID AAD28365 standard; DNA; 6904 BP.
 XX
 AC AAD28365;
 XX
 DT 22-APR-2002 (first entry)
 XX
 DE Human chemically treated genomic DNA #6.
 XX
 KM Human: cytosine methylation; neuroleptic; nootropic; antiaddictive;
 KM adrenergic alpha-1C-receptor; cytosine methylation; therapy; alcoholism;
 KM Tourette's syndrome; neurological; psychiatric; cancer; schizophrenia;
 KM drug abuse; migraine; ds.
 XX
 OS Homo sapiens.
 XX
 PN WO200202809-A2.
 XX
 PD 10-JAN-2002.
 XX
 PF 02-JUL-2001, 2001WO-EP07540.
 XX
 PR 30-JUN-2000; 2000DE-1032529.

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PR 01-SEP-2000; 2000DE-1043826.
XX
XX (EPIC-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K;
PI
XX WPI; 2002-154759/20.
XX
XX Novel nucleic acid useful for diagnosis and therapy of behavioral
PT disorder, neurological disorder and cancer, comprises a sequence of a
PT segment of chemically pretreated DNA of adrenergic alpha-1C-receptor
PT gene -
XX
XX Claim 1; Page 44-48; 190pp; English.
XX
XX The invention relates to nucleic acids comprising a segment of chemically
CC pretreated DNA of adrenergic alpha-1C-receptor gene. The invention also
CC relates to oligonucleotides or peptide nucleic acid (PNA) oligomers
CC useful for detecting cytosine methylations. The pretreated DNA is useful
CC for the diagnosis or therapy of behavioural disorders, neurological
CC disorders and cancer, in particular major depressive disorder, Tourette's
CC syndrome, schizophrenia, psychiatric and neurological disorders, smoking,
CC drug abuse, alcoholism, personality traits, compulsive gambling, human
CC immunodeficiency virus dementia, migraine, behaviours in schizophrenia
CC and schizoaffective patients, and suicidal behaviour in patients with
CC schizophrenia. The nucleic acid is useful for detecting the methylation
CC state of all Cpg dinucleotides and/or single nucleotide polymorphisms
CC (SNPs). The present sequence is human chemically treated genomic DNA.
XX
XX Sequence 6904 BP; 1326 A; 314 C; 2030 G; 3233 T; 1 other;
SQ
Query Match 100.0%; Score 21; DB 24; Length 6904;
Best Local Similarity 100.0%; Pred. No. 3.9;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GCTCATCATCCCTTCTCGCT 21
DB 1716 GCTCATCATCCCTTCTCGCT 1696

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PA (LIGG/) LIGGETT S B.
PA (SMAL/) SMALL K M.
XX
XX Liggett SB, Small KM;
PI
XX WPI; 2001-611728/70.
XX
XX P-PSDB; AAM52122.
XX
XX Genotyping an alpha-2B, 2A, or 2C adrenergic receptor gene useful for
PT determining whether an individual is at increased risk of developing a
PT disease associated with the corresponding receptor comprises detecting
PT a polymorphic site -
XX
XX Example 7; Page 151; 163pp; English.
XX
XX The invention relates to genotyping an alpha-2B, 2A, or 2C adrenergic
CC receptor gene (I)-(III) by detecting a polymorphic site, comprising;
CC (a) obtaining a sample having a polynucleotide encoding an alpha-2B,
CC alpha2A or alpha2C or fragment or complement of; and
CC (b) detecting a polymorphic site comprising nucleotide positions 901-909
CC of (I), a site comprising cytosine or guanine at position 753 of (IIIV)
CC or a site comprising (A) (ggggcgggcg) or (B) (ggggcgctgag) at
CC positions 961-972 of (III). The method may be used for genotyping an
CC alpha2B, alpha2A or alpha2C receptor gene and further used to determine
CC whether an individual is at increased risk of developing a disease
CC associated with alpha2B, alpha2A or alpha2, comprising detecting a
CC polymorphic site which correlate to disease selected from cardiovascular
CC disease, central nervous system disease and combinations of these.. In
CC addition, the technique may be used to predict an individual's response
CC to an alpha2B, alpha2A, or alpha2C agonist (e.g. epinephrine,
CC norepinephrine, clonidine, oxymetazoline, guanabenz, UK14304, BHT933 and
CC combinations of these) or antagonist (e.g. yohimbine, prazosin, ARC 239,
CC rauwolfine, idazoxan, tolazoline, phenolamine and combinations of
CC these) by detecting the polymorphic site and correlating the site to a
CC predetermined response (where the response is correlated to adenylyl
CC cyclase, MAP kinase activity, phosphorylation or inositol phosphate
CC levels). The present sequence is that of the human alpha-2AAR gene
CC (Genbank Accession AF281308).
XX
XX Sequence 1350 BP; 199 A; 490 C; 441 G; 220 T; 0 other;
SQ
Query Match 92.4%; Score 19.4; DB 23; Length 1350;
Best Local Similarity 95.2%; Pred. No. 18;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 GCTCATCATCCCTTCTCGCT 21
DB 252 GCTCATCATCCCTTCTCGCT 272

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RESULT 12
AA199917
ID AA199917 standard; DNA; 1350 BP.
XX
XX AA199917;
AC
XX 18-FEB-2002 (first entry)
DT
XX
XX Human alpha-2AAR encoding DNA.
DE
XX
XX Human; genotyping; alpha-2B; alpha-2A; alpha-2C; adrenergic receptor;
KM polymorphic site; allelic variant; cardiovascular disease;
KM central nervous system disease; adenylyl cyclase; MAP kinase activity;
KM phosphorylation; inositol phosphate; alpha-2AAR;
KM Genbank Accession AF281308; chromosome 10; de.
XX
XX Homo sapiens.
OS
XX
XX Key Location/Qualifiers
FT CDS 1..1353
FT /tag= a
FT /product= "alpha-2AAR"
XX
XX WO200179561-A2.
XX
XX 25-OCT-2001.
XX
XX 17-APR-2001; 2001WO-US12575.
XX
XX 17-APR-2000; 2000US-0551744.
XX 10-AUG-2000; 2000US-0636259.
XX 19-OCT-2000; 2000US-0692077.
XX

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RESULT 13
AA199918
ID AA199918 standard; DNA; 1350 BP.
XX
XX AA199918;
AC
XX 18-FEB-2002 (first entry)
DT
XX
XX Human alpha-2AAR variant encoding DNA.
DE
XX
XX Human; genotyping; alpha-2B; alpha-2A; alpha-2C; adrenergic receptor;
KM polymorphic site; allelic variant; cardiovascular disease;
KM central nervous system disease; adenylyl cyclase; MAP kinase activity;
KM phosphorylation; inositol phosphate; alpha-2AAR; chromosome 10; de.
XX
XX Homo sapiens.
OS
XX
XX Key Location/Qualifiers
FT CDS 1..1353
FT /tag= a
FT /product= "alpha-2AAR"
FT allele
FT replace(753,C)
FT /tag= b

```

XX WO200179561-A2.
 XX 25-OCT-2001.
 XX 17-APR-2001; 2001WO-US12575.
 XX 17-APR-2000; 2000US-0551744.
 XX 10-AUG-2000; 2000US-0636259.
 XX 19-OCT-2000; 2000US-0692077.
 XX (LIGG/) LIGGETT S B.
 XX (SMAL/) SMALL K M.
 XX Liggett SB, Small KM;
 XX WPI; 2001-611728/70.
 XX P-PSDB; AAM52123.
 XX
 XX Genotyping an alpha-2B, 2A, or 2C adrenergic receptor gene useful for
 XX determining whether an individual is at increased risk of developing a
 XX disease associated with the corresponding receptor comprises detecting
 XX a polymorphic site -
 XX
 XX Disclosure; Page 152; 163pp; English.
 XX
 XX The invention relates to genotyping an alpha-2B, 2A, or 2C adrenergic
 XX receptor gene (I)-(III) by detecting a polymorphic site, comprising;
 XX (a) obtaining a sample having a polynucleotide encoding an alpha-2B,
 XX alpha2A or alpha2C or fragment or complement of; and
 XX (b) detecting a polymorphic site comprising nucleotide positions 901-909
 XX of (I), a site comprising cytosine or guanine at position 753 of (IIIV)
 XX or a site comprising (A) (959GCG959CG) or (B) (959GCG959CG) at
 XX positions 961-972 of (III). The method may be used for genotyping an
 XX alpha2B, alpha2A or alpha2C receptor gene and further used to determine
 XX whether an individual is at increased risk of developing a disease
 XX associated with alpha2B, alpha2A or alpha2, comprising detecting a
 XX polymorphic site which correlate to disease selected from cardiovascular
 XX disease, central nervous system disease and combinations of these. In
 XX addition, the technique may be used to predict an individual's response
 XX to an alpha2B, alpha2A, or alpha2C agonist (e.g. epinephrine,
 XX norepinephrine, clonidine, oxymetazoline, guanabenz, UK14304, BHT933 and
 XX combinations of these) or antagonist (e.g. yohimbine, prazosin, ARC 239,
 XX rauwolfine, idazoxan, tolazoline, phenolamine and combinations of
 XX these) by detecting the polymorphic site and correlating the site to a
 XX predetermined response (where the response is correlated to adenylyl
 XX cyclase, MAP kinase activity, phosphorylation or inositol phosphate
 XX levels). The present sequence is that of the human alpha-2AAR variant
 XX gene.
 XX
 XX Sequence 1350 BP; 199 A; 489 C; 442 G; 220 T; 0 other;
 XX
 XX Query Match 92.4%; Score 19.4; DB 23; Length 1350;
 XX Best Local Similarity 95.2%; Pred. No. 18;
 XX Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 XX
 XX 1 GCTGATCATCCCTTTCGCT 21
 XX |||||
 XX Db 252 GCTGATCATCCCTTTCGCT 272
 XX
 XX RESULT 14
 XX ABO47500/c
 XX ID ABO47500 standard; DNA; 1733 BP.
 XX AC ABO47500;
 XX
 XX 12-JUL-2002 (first entry)
 XX
 XX Oligonucleotide for detecting cytosine methylation SEQ ID NO 34091.
 XX Human; cytosine methylation; 5'-CpG-3'; uracil; cytosine; diagnosis;
 XX drug; side effect; cancer; central nervous system; cardiovascular;
 XX

KW gastrointestinal; respiratory system; single nucleotide polymorphism;
 KW SNP; cell differentiation; ds.
 XX Homo sapiens.
 XX WO200218632-A2.
 XX 07-MAR-2002.
 XX
 XX 01-SEP-2001; 2001WO-EP10074.
 XX
 XX 01-SEP-2000; 2000DE-1043826.
 XX 05-SEP-2000; 2000DE-1044543.
 XX
 XX (EPIC-) EPIGENOMICS AG.
 XX
 XX Olek A, Piepenbrock C, Berlin K, Guectig D;
 XX WPI; 2002-371829/40.
 XX
 XX Determining the degree of cytosine methylation in genomic DNA, useful
 XX for diagnosis and prognosis, comprises selective hybridization of
 XX amplicons from chemically treated DNA -
 XX
 XX Claim 12; 56pp + Sequence Listing; 56pp; German.
 XX
 XX This invention describes a novel method for determining the degree of
 XX methylation of a particular cytosine in a motif 5'-CpG-3', present in a
 XX genomic sample of DNA. The sample is treated chemically to convert in a
 XX cytosine (C) but not methylated C, to uracil, then part of the genomic
 XX DNA that contains the target C is amplified to form a labeled amplicon.
 XX The amplicon is hybridised to two classes, each with at least one
 XX member, of oligonucleotides and/or peptide-nucleic acid (PNA) oligomers
 XX and the degree of hybridisation to both classes is determined from the
 XX label on the amplicon. From the ratio of labels hybridised to the two
 XX classes of oligomers, the degree of methylation is calculated. The method
 XX is used: (i) for diagnosis and/or prognosis of side effects of
 XX therapeutic drugs and of a wide range of diseases, e.g. cancer, disorders
 XX of the central nervous, cardiovascular, gastrointestinal and respiratory
 XX systems etc., particularly by detecting mutations or single nucleotide
 XX polymorphisms (SNP's); and (ii) for differentiation of cell or tissue
 XX types and for investigating cell differentiation. The method allows the
 XX methylation status of many C residues to be determined simultaneously.
 XX ABO13410-ABO94121 represent genomic DNA sequences used to illustrate the
 XX method for determining the degree of cytosine methylation described in
 XX the disclosure of the invention.
 XX
 XX Sequence 1733 BP; 271 A; 211 C; 625 G; 626 T; 0 other;
 XX
 XX Query Match 92.4%; Score 19.4; DB 24; Length 1733;
 XX Best Local Similarity 95.2%; Pred. No. 18;
 XX Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 XX
 XX 1 GCTGATCATCCCTTTCGCT 21
 XX |||||
 XX Db 1222 GCTGATCATCCCTTTCGCT 1202
 XX
 XX RESULT 15
 XX ABO47501
 XX ID ABO47501 standard; DNA; 1733 BP.
 XX AC ABO47501;
 XX
 XX 12-JUL-2002 (first entry)
 XX
 XX Oligonucleotide for detecting cytosine methylation SEQ ID NO 34092.
 XX Human; cytosine methylation; 5'-CpG-3'; uracil; cytosine; diagnosis;
 KW drug; side effect; cancer; central nervous system; cardiovascular;
 KW gastrointestinal; respiratory system; single nucleotide polymorphism;
 KW SNP; cell differentiation; ds.
 XX

OS Homo sapiens.
 XX
 PN WO200218632-A2.
 XX
 PD 07-MAR-2002.
 XX
 PF 01-SEP-2001; 2001WO-EP10074.
 XX
 PR 01-SEP-2000; 2000DE-1043826.
 PR 05-SEP-2000; 2000DE-1044543.
 XX
 PA (EPIC-) EPIGENOMICS AG.
 XX
 PI Olek A, Piepenbrock C, Berlin K, Guettig D;
 XX
 DR WPI; 2002-371829/40.
 XX
 PT Determining the degree of cytosine methylation in genomic DNA, useful
 PT for diagnosis and prognosis, comprises selective hybridization of
 PT amplicons from chemically treated DNA -
 XX
 PS Claim 12; 56pp + Sequence Listing; 56pp; German.
 XX
 CC This invention describes a novel method for determining the degree of
 CC methylation of a particular cytosine in a motif 5'-CpG-3', present in a
 CC genomic sample of DNA. The sample is treated chemically to convert
 CC cytosine (C) but not methylated C, to uracil, then part of the genomic
 CC DNA that contains the target C is amplified to form a labeled amplicon.
 CC The amplicon is hybridised to two classes, each with at least one
 CC member, of oligonucleotides and/or peptide-nucleic acid (PNA) oligomers
 CC and the degree of hybridisation to both classes is determined from the
 CC label on the amplicon. From the ratio of labels hybridised to the two
 CC classes of oligomers, the degree of methylation is calculated. The method
 CC is used: (i) for diagnosis and/or prognosis of side effects of
 CC therapeutic drugs and of a wide range of diseases, e.g. cancer, disorders
 CC of the central nervous, cardiovascular, gastrointestinal and respiratory
 CC systems etc., particularly by detecting mutations or single nucleotide
 CC polymorphisms (SNP/s); and (ii) for differentiation of cell or tissue
 CC types and for investigating cell differentiation. The method allows the
 CC methylation status of many C residues to be determined simultaneously.
 CC ABQ13410-ABQ54121 represent genomic DNA sequences used to illustrate the
 CC method for determining the degree of cytosine methylation described in
 CC the disclosure of the invention.
 XX
 SQ Sequence 1733 BP; 626 A; 625 C; 211 G; 271 T; 0 other;

Query Match 92.4%; Score 19.4; DB 24; Length 1733;
 Best Local Similarity 95.2%; Pred. No. 18;
 Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GCTCATCATCCCTTCTCGCT 21
 |||||
 DB 512 GCTGTCATCATCCCTTCTCGCT 532

Search completed: February 12, 2004, 04:01:23
 Job time : 111.378 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using SW model

Run on: February 12, 2004, 04:01:41 ; Search time 28.6829 Seconds
(without alignments)
323.156 Million cell updates/sec

Title: US-09-692-077D-13

Perfect score: 21

Sequence: 1 gctcatcctccctccgcct 21

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued_Patents_NA:*
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2: /cgn2_6/prodata/2/1na/5B_COMB.seq:*
3: /cgn2_6/prodata/2/1na/6A_COMB.seq:*
4: /cgn2_6/prodata/2/1na/6B_COMB.seq:*
5: /cgn2_6/prodata/2/1na/PCUS_COMB.seq:*
6: /cgn2_6/prodata/2/1na/backfile1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	21	100.0	2072	4	US-09-016-434-1181 Sequence 1181, Ap
2	19.4	92.4	3604	4	US-09-016-434-1180 Sequence 1180, Ap
3	18.4	87.6	297	4	US-09-313-294A-1953 Sequence 1953, Ap
4	16.8	80.0	967	3	US-09-248-335-51 Sequence 51, Appl
5	16.8	80.0	1500	4	US-09-252-991A-16352 Sequence 16352, A
6	16.8	80.0	1584	4	US-09-252-991A-16239 Sequence 16239, A
7	16.4	78.1	2102	1	US-08-784-651-5 Sequence 5, Appl
8	16.2	77.1	1860	4	US-09-489-847-53 Sequence 53, Appl
9	16.2	77.1	2837	2	US-08-993-228-11 Sequence 11, Appl
10	16	76.2	3430	4	US-09-462-561B-9 Sequence 9, Appl
11	15.8	75.2	1222	4	US-09-511-625B-21 Sequence 21, Appl
12	15.8	75.2	1322	4	US-09-634-238-178 Sequence 178, Appl
13	15.8	75.2	2168	1	US-08-784-651-1 Sequence 1, Appl
14	15.8	75.2	2323	4	US-09-342-647-17 Sequence 17, Appl
15	15.8	75.2	17425	4	US-09-511-625B-5 Sequence 5, Appl
16	15.4	73.3	8532	1	US-08-452-655B-1 Sequence 1, Appl
17	15.4	73.3	8532	1	US-08-450-582-1 Sequence 1, Appl
18	15.4	73.3	9606	1	US-07-741-940-1 Sequence 1, Appl
19	15.4	73.3	9606	1	US-08-289-548A-1 Sequence 1, Appl
20	15.4	73.3	9606	1	US-08-452-654-1 Sequence 1, Appl
21	15.4	73.3	9606	2	US-08-370-235A-1 Sequence 1, Appl
22	15.4	73.3	9606	4	US-08-449-731-1 Sequence 1, Appl
23	15.4	73.3	580073	4	US-08-545-528B-1 Sequence 1, Appl
24	15.2	72.4	2573	4	US-09-620-312D-609 Sequence 609, Appl
25	15.2	72.4	4344	4	US-09-462-561B-11 Sequence 11, Appl
26	15.2	72.4	6545	5	PCT-US95-13749-3 Sequence 3, Appl
27	15.2	72.4	8815	4	US-09-687-731-12 Sequence 12, Appl

C 28	15.2	72.4	36519	3	US-08-923-137-2	Sequence 2, Appl
29	15.2	72.4	4403765	3	US-09-103-840A-2	Sequence 2, Appl
30	15.2	72.4	4411529	3	US-09-103-840A-1	Sequence 1, Appl
C 31	14.8	70.5	155	3	US-08-444-818-1	Sequence 1, Appl
C 32	14.8	70.5	155	3	US-08-444-818-3	Sequence 3, Appl
C 33	14.8	70.5	164	3	US-08-444-818-6	Sequence 6, Appl
C 34	14.8	70.5	318	3	US-08-444-818-5	Sequence 5, Appl
C 35	14.8	70.5	353	3	US-08-444-818-4	Sequence 4, Appl
C 36	14.8	70.5	353	3	US-08-444-818-9	Sequence 9, Appl
C 37	14.8	70.5	387	3	US-08-444-818-7	Sequence 7, Appl
C 38	14.8	70.5	617	3	US-09-146-222-9	Sequence 9, Appl
C 39	14.8	70.5	712	3	US-08-444-818-13	Sequence 13, Appl
C 40	14.8	70.5	943	2	US-08-483-695-6	Sequence 6, Appl
C 41	14.8	70.5	943	2	US-08-483-695-43	Sequence 43, Appl
C 42	14.8	70.5	943	2	US-07-965-285-6	Sequence 6, Appl
C 43	14.8	70.5	943	2	US-07-965-285-43	Sequence 43, Appl
C 44	14.8	70.5	943	2	US-08-487-231-6	Sequence 6, Appl
C 45	14.8	70.5	943	2	US-08-487-231-43	Sequence 43, Appl

ALIGNMENTS

RESULT 1
US-09-016-434-1181
; Sequence 1181, Application US/09016434
; Patent No. 6500938
; GENERAL INFORMATION:
; APPLICANT: Janice Au-Young
; APPLICANT: Jeffrey J. Seilhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
; TITLE OF INVENTION: PATHWAY GENE EXPRESSION
; NUMBER OF SEQUENCES: 1490
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/016,434
; FILING DATE: HEREWITH
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, Karen J.
; REGISTRATION NUMBER: 37,071
; REFERENCE/DOCKET NUMBER: PA-0002 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 1181:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2072 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GENBANK
; CLONE: g178197
; US-09-016-434-1181
Query Match 100.0%; Score 21; DB 4; Length 2072;
Best Local Similarity 100.0%; Pred. No. 0.48;

ORGANISM: *Pseudomonas aeruginosa*

US-09-252-991A-16352

Query Match 80.0%; Score 16.8; DB 4; Length 1500;
Best Local Similarity 90.0%; Pred. No. 42;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GCTCATCATCCTTCTCGC 20
DB 1434 GCTCATCACCCCTTCTCGC 1415

RESULT 6
US-09-252-991A-16239
Sequence 16239, Application US/09252991A
Patent No. 6551795

GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 16239
LENGTH: 1584
TYPE: DNA
ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-16239

Query Match 80.0%; Score 16.8; DB 4; Length 1584;
Best Local Similarity 90.0%; Pred. No. 42;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GCTCATCATCCTTCTCGC 20
DB 124 GCTCATCACCCCTTCTCGC 143

RESULT 7
US-08-784-651-5/C

Sequence 5, Application US/08784651
Patent No. 5821102
GENERAL INFORMATION:
APPLICANT: Berka, Randy
APPLICANT: Boomhathan, Karuppan
APPLICANT: Sandai, Thomas
TITLE OF INVENTION: Nucleic Acids Encoding Polypeptides
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 58211020 No. 5821102disk of No. 5821102th America, Inc.
STREET: 405 Lexington Avenue
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10174
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: PASTE9 for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/784,651
FILING DATE: 21-JAN-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Agtis, Cheryl H.
REGISTRATION NUMBER: 34,086
REFERENCE/DOCKET NUMBER: 4608.200-US
TELECOMMUNICATION INFORMATION:

TELEPHONE: 212-867-0123
TELEFAX: 212-878-9655
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 2102 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: Genomic DNA
US-08-784-651-5

Query Match 78.1%; Score 16.4; DB 1; Length 2102;
Best Local Similarity 94.4%; Pred. No. 68;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 TCATCATCCCTTCTCGC 20
DB 336 TCATCATCCCTTCTCGC 319

RESULT 8
US-09-489-847-53/C

Sequence 53, Application US/09489847
Patent No. 6476195
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: 98 Human Secreted Proteins
FILE REFERENCE: P2031P1
CURRENT APPLICATION NUMBER: US/09/489,847
CURRENT FILING DATE: 2000-01-24
EARLIER APPLICATION NUMBER: PCT/US99/17130
EARLIER FILING DATE: 1999-07-29
EARLIER APPLICATION NUMBER: 60/094,657
EARLIER FILING DATE: 1998-07-30
EARLIER APPLICATION NUMBER: 60/095,486
EARLIER FILING DATE: 1998-08-05
EARLIER APPLICATION NUMBER: 60/096,319
EARLIER FILING DATE: 1998-08-12
EARLIER APPLICATION NUMBER: 60/095,454
EARLIER FILING DATE: 1998-08-06
EARLIER APPLICATION NUMBER: 60/095,455
EARLIER FILING DATE: 1998-08-06
NUMBER OF SEQ ID NOS: 376
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 53
LENGTH: 1860
TYPE: DNA
ORGANISM: Homo sapiens
US-09-489-847-53

Query Match 77.1%; Score 16.2; DB 4; Length 1860;
Best Local Similarity 85.7%; Pred. No. 82;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GCTCATCATCCTTCTCGC 21
DB 38 GCTCATCATCCTTCTCGC 18

RESULT 9
US-08-993-228-11

Sequence 11, Application US/08993228
Patent No. 5976838
GENERAL INFORMATION:
APPLICANT: Jacobs, Kenneth
APPLICANT: McCoy, John M.
APPLICANT: LaValle, Edward R.
APPLICANT: Racie, Lisa A.
APPLICANT: Merberg, David
APPLICANT: Treacy, Maurice
APPLICANT: Spaulding, Vikki
APPLICANT: Agostino, Michael J.
TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES

```

; TITLE OF INVENTION: ENCODING THEM
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc.
; STREET: 87 Cambridgepark Drive
; CITY: Cambridge
; STATE: MA
; COUNTRY: U.S.A.
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/993,228
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Sprunger, Suzanne A.
; REGISTRATION NUMBER: 41,323
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 498-8284
; TELEFAX: (617) 876-5851
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2837 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; US-08-993-228-11

Query Match
Best Local Similarity 77.1%; Score 16.2; DB 2; Length 2837;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GCTCATCATCCCTTCTCGCT 21
Db 625 GCTCATCATCCCTTCTCTCT 645

RESULT 10
US-09-462-561B-9/c
; Sequence 9, Application US/09462561B
; Patent No. 6455252
; GENERAL INFORMATION:
; APPLICANT: Made, Nicholas M.
; APPLICANT: Harrison, Bruce T.
; APPLICANT: King, Brian W.
; APPLICANT: Reed, Kenneth C.
; APPLICANT: Murphy, Kathleen M.
; TITLE OF INVENTION: DETERMINATION OF GENETIC SEX IN EQUINE SPECIES BY
; FILE REFERENCE: Made et al
; CURRENT APPLICATION NUMBER: US/09/462,561B
; PRIOR FILING DATE: 2000-03-22
; PRIOR APPLICATION NUMBER: P07802
; PRIOR FILING DATE: 1997-07-09
; PRIOR APPLICATION NUMBER: PCT/AU98/00533
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 9
; LENGTH: 3430
; TYPE: DNA
; ORGANISM: Equus caballus
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1110)
; OTHER INFORMATION: n at position 1110 = a, t, c, or g
; NAME/KEY: unsure
; LOCATION: (1656)

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; OTHER INFORMATION: n at position 1656 = a, t, c, or g
; NAME/KEY: unsure
; LOCATION: (1658)
; OTHER INFORMATION: n at position 1658 = a, t, c, or g
; NAME/KEY: unsure
; LOCATION: (1995)
; OTHER INFORMATION: n at position 1995 = a, t, c, or g
; NAME/KEY: unsure
; LOCATION: (2087)
; OTHER INFORMATION: n at position 2087 = a, t, c, or g
; NAME/KEY: unsure
; LOCATION: (2781)
; OTHER INFORMATION: n at position 2781 = a, t, c, or g
; US-09-462-561B-9

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Query Match
Best Local Similarity 76.2%; Score 16; DB 4; Length 3430;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy 2 CTCATCATCCCTTCTC 18
Db 2089 CTATCATCCCTTCTC 2073

RESULT 11
US-09-511-625B-21/c
; Sequence 21, Application US/09511625B
; Patent No. 6368828
; GENERAL INFORMATION:
; APPLICANT: Laroche, William J.
; APPLICANT: Patel, Bhavvin
; APPLICANT: Pierce, Jacalyn H.
; TITLE OF INVENTION: ATTENUATED AND DOMINANT NEGATIVE VARIANT
; FILE REFERENCE: 14014.0300u1
; CURRENT APPLICATION NUMBER: US/09/511,625B
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: PCT/US98/17821
; PRIOR FILING DATE: 1998-08-27
; PRIOR APPLICATION NUMBER: 60/070,397
; PRIOR FILING DATE: 1998-01-05
; PRIOR APPLICATION NUMBER: 60/056,075
; PRIOR FILING DATE: 1997-08-27
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 21
; LENGTH: 414
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of artificial Sequence: /No. 6368828e -
; US-09-511-625B-21

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Query Match
Best Local Similarity 75.2%; Score 15.8; DB 4; Length 414;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 TCATCATCCCTTCTCGCT 21
Db 340 TCAGCATCCCTTCTCTCT 322

RESULT 12
US-09-634-238-178/c
; Sequence 178, Application US/09634238
; Patent No. 6344772
; GENERAL INFORMATION:
; APPLICANT: Glenn, Matthew
; APPLICANT: Havukala, Ilka J.
; APPLICANT: Bloksberg, Leonard, N.
; APPLICANT: Lubbers, Mark W.
; APPLICANT: Dekker, James

```

APPLICANT: Christenson, Anna C.
APPLICANT: Holland, Ross
APPLICANT: O'Toole, Paul W.
APPLICANT: Reid, Julian R.
APPLICANT: Coolbear, Timothy
TITLE OF INVENTION: Polynucleotides, materials incorporating
FILE REFERENCE: 11000.1043U1
CURRENT APPLICATION NUMBER: US/09/634,238
CURRENT FILING DATE: 2000-08-08
NUMBER OF SEQ ID NOS: 422
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 178
LENGTH: 1322
TYPE: DNA
ORGANISM: Lactobacillus rhamnosus
US-09-634-238-178

Query Match 75.2%; Score 15.8; DB 4; Length 1322;
Best Local Similarity 89.5%; Pred. No. 1.2e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 3 TCATCATCCCTTTCGCT 21
Db 288 TCATCATCCGTTTCGCT 270

RESULT 13
US-08-784-651-1/c
Sequence 1, Application US/08784651
Patent No. 5821102
GENERAL INFORMATION:
APPLICANT: Berka, Randy
APPLICANT: Boomnathan, Karuppan
APPLICANT: Sandal, Thomas
TITLE OF INVENTION: Nucleic Acids Encoding Polypeptides
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSER: No. 58211020 No. 5821102disk of No. 5821102ch America, Inc.
STREET: 405 Lexington Avenue
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10174
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/784,651
FILING DATE: 21-JAN-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Agria, Cheryl H.
REGISTRATION NUMBER: 34,086
REFERENCE/DOCKET NUMBER: 4608.200-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
TELEFAX: 212-878-9655
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2168 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: Genomic DNA
US-08-784-651-1

Query Match 75.2%; Score 15.8; DB 1; Length 2168;
Best Local Similarity 89.5%; Pred. No. 1.3e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 CTCATCATCCCTTTCGCG 20
Db 346 CTCACATCCGTTTCGCG 328

RESULT 14
US-09-342-647-17
Sequence 17, Application US/09342647A
Patent No. 6368840
GENERAL INFORMATION:
APPLICANT: Canoon, Edgar B.
APPLICANT: Canoon, Rebecca E.
APPLICANT: Hiltz, William D.
APPLICANT: Kinney, Anthony J.
TITLE OF INVENTION: ACYL-COA Oxidase Homologs
FILE REFERENCE: BR-1175
CURRENT APPLICATION NUMBER: US/09/342,647A
CURRENT FILING DATE: 1999-06-29
EARLIER APPLICATION NUMBER: 60/092,482
EARLIER FILING DATE: 1998-07-10
NUMBER OF SEQ ID NOS: 31
SOFTWARE: Microsoft Office 97
SEQ ID NO 17
LENGTH: 2323
TYPE: DNA
ORGANISM: Oryza sativa
US-09-342-647-17

Query Match 75.2%; Score 15.8; DB 4; Length 2323;
Best Local Similarity 89.5%; Pred. No. 1.3e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 TCATCATCCCTTTCGCT 21
Db 2064 TCATCTCCCTTTCGCT 2082

RESULT 15
US-09-511-625B-5/c
Sequence 5, Application US/09511625B
Patent No. 6368828
GENERAL INFORMATION:
APPLICANT: Larocheille, William J.
APPLICANT: Patel, Bhavin
APPLICANT: Pierce, Jacalyn H.
TITLE OF INVENTION: ATTENUATED AND DOMINANT NEGATIVE VARIANT
FILE REFERENCE: 14014.0300u1
CURRENT APPLICATION NUMBER: US/09/511,625B
CURRENT FILING DATE: 2000-02-23
PRIOR APPLICATION NUMBER: PCT/US98/17821
PRIOR FILING DATE: 1998-08-27
PRIOR APPLICATION NUMBER: 60/070,397
PRIOR FILING DATE: 1998-01-05
PRIOR APPLICATION NUMBER: 60/056,075
PRIOR FILING DATE: 1997-08-27
NUMBER OF SEQ ID NOS: 70
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 5
LENGTH: 17425
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of artificial Sequence:/No. 6368828e -
NAME/KEY: misc feature
LOCATION: (1)... (17425)
OTHER INFORMATION: n = a, c, c or g
US-09-511-625B-5

Query Match 75.2%; Score 15.8; DB 4; Length 17425;
Best Local Similarity 89.5%; Pred. No. 1.7e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Sun Feb 15 07:29:41 2004

us-09-692-077d-13.rn1

Page 6

Oy 3 TCATCATCCCTTCTCGCT 21
Db 6790 TCAGCATTCCTTCTCGCT 6772

Search completed: February 12, 2004, 06:07:47
Job time : 40.6829 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Comphen Ltd.

OM nucleic - nucleic search, using SW model

Run on: February 12, 2004, 04:42:03 ; Search time 119.341 Seconds
(without alignments)
648.193 Million cell updates/sec

Title: US-09-692-077d-13

Perfect score: 21
Sequence: 1 GCTCATCATCCCTTCTCGCT 21

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 2449703 seqs, 1841816367 residues

Total number of hits satisfying chosen parameters: 4899406

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Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Published Applications_NA.*
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17: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
18: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	21	100.0	21	US-10-001-073-13	Sequence 13, Appl
2	21	100.0	1344	9 US-09-825-923-1	Sequence 1, Appl
3	21	100.0	1344	15 US-10-077-870-1	Sequence 1, Appl
4	21	100.0	1344	15 US-10-001-073-2	Sequence 2, Appl
5	21	100.0	1353	9 US-09-825-923-3	Sequence 3, Appl
6	21	100.0	1353	15 US-10-077-870-3	Sequence 3, Appl
7	21	100.0	1353	15 US-10-001-073-1	Sequence 1, Appl
8	21	100.0	3274	15 US-10-305-720-1181	Sequence 1181, Ap
9	21	100.0	3274	15 US-10-305-720-1181	Sequence 1181, Ap
10	21	100.0	6904	13 US-10-311-455-48	Sequence 48, Appl
11	21	100.0	6904	13 US-10-311-455-48	Sequence 48, Appl
12	19.4	92.4	1350	15 US-10-001-073-24	Sequence 24, Appl
13	19.4	92.4	1350	15 US-10-001-073-25	Sequence 25, Appl
14	19.4	92.4	3604	12 US-10-305-720-1180	Sequence 1180, Ap
15	19.4	92.4	3653	15 US-10-311-455-46	Sequence 39, Appl
15	19.4	92.4	7353	13 US-10-311-455-46	Sequence 46, Appl

16	17.4	82.9	96588	12 US-10-085-117-64	Sequence 64, Appl
17	17	81.0	688	13 US-10-027-632-173743	Sequence 173743, Sequence 173743, Sequence 173743, Sequence 224986, Sequence 224986, Sequence 224986, Sequence 480, App
18	17	81.0	688	13 US-10-027-632-173743	Sequence 480, App
19	16.8	80.0	628	13 US-10-027-632-224986	Sequence 224986, Sequence 224986, Sequence 224986, Sequence 480, App
20	16.8	80.0	628	14 US-10-027-632-224986	Sequence 480, App
21	16.4	78.1	954	10 US-09-886-055-480	Sequence 480, App
22	16.4	78.1	954	11 US-09-804-291-480	Sequence 13, Appl
23	16.4	78.1	954	11 US-09-804-291-480	Sequence 13, Appl
24	16.4	78.1	954	11 US-09-804-291-480	Sequence 13, Appl
25	16.4	78.1	954	11 US-09-804-291-480	Sequence 13, Appl
26	16.4	78.1	958	13 US-10-025-806-53	Sequence 29, Appl
27	16.4	78.1	958	13 US-10-025-806-53	Sequence 53, Appl
28	16.4	78.1	958	13 US-09-965-422-31	Sequence 31, Appl
29	16.4	78.1	958	13 US-09-965-422-31	Sequence 31, Appl
30	16.4	78.1	1017	10 US-09-886-055-428	Sequence 428, App
31	16.4	78.1	1017	10 US-09-886-055-428	Sequence 428, App
32	16.4	78.1	1354	12 US-10-292-798-1	Sequence 1, Appl
33	16.4	78.1	1354	12 US-10-292-798-1	Sequence 1, Appl
34	16.4	78.1	2631	10 US-09-801-368-43	Sequence 43, Appl
35	16.4	78.1	2631	10 US-09-801-368-43	Sequence 43, Appl
36	16.2	77.1	268	9 US-09-294-093B-2749	Sequence 2749, Ap
37	16.2	77.1	509	12 US-10-260-238-3223	Sequence 3223, Ap
38	16.2	77.1	540	10 US-09-974-300-6869	Sequence 6869, Ap
39	16.2	77.1	689	13 US-10-027-632-134859	Sequence 134859, Sequence 134859, Sequence 134859, Sequence 14649, A
40	16.2	77.1	689	14 US-10-027-632-134859	Sequence 14649, A
41	16.2	77.1	714	14 US-10-027-632-14649	Sequence 124, App
42	16.2	77.1	966	11 US-09-886-055-124	Sequence 124, App
43	16.2	77.1	966	11 US-09-886-055-124	Sequence 124, App
44	16.2	77.1	1121	13 US-09-844-861A-3	Sequence 3, Appl
45	16.2	77.1	1311	12 US-10-369-493-28507	Sequence 28507, A

ALIGNMENTS

RESULT 1
US-10-001-073-13
; Sequence 13, Application US/10001073
; Publication No. US20030113725A1
; GENERAL INFORMATION:
; APPLICANT: Liggett, Stephen
; APPLICANT: Small, Kirsten
; TITLE OF INVENTION: Alpha-2-adrenergic receptor polymorphisms
; FILE REFERENCE: 13073-PCT
; CURRENT APPLICATION NUMBER: US/10/001-073
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 13
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-001-073-13

Query Match 100.0%; Score 21; DB 15; Length 21;
Best Local Similarity 100.0%; Pred. No. 3.1; Indels 0; Gaps 0;
Matches 21; Conservative 0; Mismatches 0

QY 1 GCTCATCATCCCTTCTCGCT 21
DB 1 GCTCATCATCCCTTCTCGCT 21

RESULT 2
US-09-825-923-1
; Sequence 1, Application US/09825923
; Patent No. US20010016338A1
; GENERAL INFORMATION:
; APPLICANT: Snagit, Amir
; APPLICANT: Heimonen, Paula
; APPLICANT: Alhopuro, Pia
; APPLICANT: Karvonen, Matti
; APPLICANT: Koulu, Markku

APPLICANT: Pesonen, Ullamari
APPLICANT: Scheinin, Mika
APPLICANT: Salonen, Jukka T
APPLICANT: Tuomala, Tomi-Pekka
APPLICANT: Lakka, Timo A
APPLICANT: Nyyssönen, Kristiina
APPLICANT: Salonen, Riitta
APPLICANT: Kaunonen, Jussi
APPLICANT: Valkonen, Veli-Pekka
TITLE OF INVENTION: A DNA molecule encoding a variant alpha-2B-adrenoceptor
FILE REFERENCE: Alpha-2B-AR variant
CURRENT APPLICATION NUMBER: US/09/825,923
PRIOR FILING DATE: 2001-04-05
PRIOR FILING DATE: 09/422,985
NUMBER OF SEQ ID NOS: 10
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1
LENGTH: 1344
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (1)..(1341)
OTHER INFORMATION: Coding sequence for variant human
OTHER INFORMATION: alpha-2B-adrenoceptor protein
US-09-825-923-1

Query Match 100.0%; Score 21; DB 9; Length 1344;
Best Local Similarity 100.0%; Pred. No. 3.8;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCATCATCCCTTCTCGCT 21
DB 189 GCTCATCATCCCTTCTCGCT 209

RESULT 3
US-10-077-870-1
Sequence 1, Application US/10077870
Publication No. US2003003470A1
GENERAL INFORMATION:
APPLICANT: Salonen, Jukka T
TITLE OF INVENTION: Method for detecting a risk of hypertension and uses thereof
FILE REFERENCE: 0933-0183P
CURRENT APPLICATION NUMBER: US/10/077,870
PRIOR FILING DATE: 2002-05-21
PRIOR APPLICATION NUMBER: FI 20010323
PRIOR FILING DATE: 2001-02-20
NUMBER OF SEQ ID NOS: 10
SOFTWARE: PatentIn Ver. 3.1
SEQ ID NO 1
LENGTH: 1344
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (1)..(1341)
OTHER INFORMATION: Coding sequence for variant human alpha-2B-adrenoceptor protein
US-10-077-870-1

Query Match 100.0%; Score 21; DB 15; Length 1344;
Best Local Similarity 100.0%; Pred. No. 3.8;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCATCATCCCTTCTCGCT 21
DB 189 GCTCATCATCCCTTCTCGCT 209

RESULT 4
US-10-001-073-2

Sequence 2, Application US/10001073
Publication No. US20030113725A1
GENERAL INFORMATION:
APPLICANT: Liggett, Stephen
APPLICANT: Small, Kirsten
TITLE OF INVENTION: Alpha-2-adrenergic receptor polymorphisms
FILE REFERENCE: 13073-PCT
CURRENT APPLICATION NUMBER: US/10/001,073
CURRENT FILING DATE: 2001-11-01
NUMBER OF SEQ ID NOS: 53
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2
LENGTH: 1344
TYPE: DNA
ORGANISM: Homo sapiens
US-10-001-073-2

Query Match 100.0%; Score 21; DB 15; Length 1344;
Best Local Similarity 100.0%; Pred. No. 3.8;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCATCATCCCTTCTCGCT 21
DB 189 GCTCATCATCCCTTCTCGCT 209

RESULT 5
US-09-825-923-3
Sequence 3, Application US/09825923
Patent No. US20010016338A1
GENERAL INFORMATION:
APPLICANT: Snapir, Amir
APPLICANT: Heinonen, Paula
APPLICANT: Alhopuro, Pia
APPLICANT: Karvonen, Matti
APPLICANT: Koulu, Markku
APPLICANT: Pesonen, Ullamari
APPLICANT: Scheinin, Mika
APPLICANT: Salonen, Jukka T
APPLICANT: Tuomala, Tomi-Pekka
APPLICANT: Lakka, Timo A
APPLICANT: Nyyssönen, Kristiina
APPLICANT: Salonen, Riitta
APPLICANT: Kaunonen, Jussi
APPLICANT: Valkonen, Veli-Pekka
TITLE OF INVENTION: A DNA molecule encoding a variant alpha-2B-adrenoceptor
FILE REFERENCE: Alpha-2B-AR variant
CURRENT APPLICATION NUMBER: US/09/825,923
PRIOR FILING DATE: 2001-04-05
PRIOR APPLICATION NUMBER: 09/422,985
NUMBER OF SEQ ID NOS: 10
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 3
LENGTH: 1353
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (1)..(1350)
OTHER INFORMATION: Coding sequence for human alpha-2B-adrenoceptor
OTHER INFORMATION: protein
US-09-825-923-3

Query Match 100.0%; Score 21; DB 9; Length 1353;
Best Local Similarity 100.0%; Pred. No. 3.8;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCATCATCCCTTCTCGCT 21
DB 189 GCTCATCATCCCTTCTCGCT 209

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RESULT 6
US-10-077-870-3
; Sequence 3, Application US/10077870
; Publication No. US20030003470A1
; GENERAL INFORMATION:
; APPLICANT: Salonen, Jukka T
; TITLE OF INVENTION: Method for detecting a risk of hypertension and uses thereof
; FILE REFERENCE: 0933-0183P
; CURRENT APPLICATION NUMBER: US/10/077,870
; CURRENT FILING DATE: 2002-05-21
; PRIOR APPLICATION NUMBER: FI 20010323
; PRIOR FILING DATE: 2001-02-20
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 3.1
; SEQ ID NO 3
; LENGTH: 1353
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1350)
; OTHER INFORMATION: Coding sequence for human alpha-2B-adrenoceptor protein
US-10-077-870-3

Query Match          100.0%; Score 21; DB 15; Length 1353;
Best Local Similarity 100.0%; Pred. No. 3.8;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCATCATCCCTTCTCGCT 21
DB 189 GCTCATCATCCCTTCTCGCT 209

RESULT 7
US-10-001-073-1
; Sequence 1, Application US/10001073
; Publication No. US20030113725A1
; GENERAL INFORMATION:
; APPLICANT: Liggett, Stephen
; APPLICANT: Small, Kirsten
; TITLE OF INVENTION: Alpha-2-adrenergic receptor polymorphisms
; FILE REFERENCE: 13073-PCT
; CURRENT APPLICATION NUMBER: US/10/001,073
; CURRENT FILING DATE: 2001-11-01
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 1353
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-001-073-1

Query Match          100.0%; Score 21; DB 15; Length 1353;
Best Local Similarity 100.0%; Pred. No. 3.8;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCATCATCCCTTCTCGCT 21
DB 189 GCTCATCATCCCTTCTCGCT 209

RESULT 8
US-10-305-720-1181
; Sequence 1181, Application US/10305720
; Publication No. US20040010136A1
; GENERAL INFORMATION:
; APPLICANT: Au-Yang, Janice K.; Sellhammer, Jeffrey J.
; TITLE OF INVENTION: Composition for the Detection of Signaling Pathway Gene Expression
; FILE REFERENCE: PA-0002-1 CON
; CURRENT APPLICATION NUMBER: US/10/305,720
; CURRENT FILING DATE: 2002-11-26
; PRIOR APPLICATION NUMBER: 09/016,434
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; PRIOR FILING DATE: 1998-01-30
; NUMBER OF SEQ ID NOS: 1490
; SOFTWARE: PERL Program
; SEQ ID NO 1181
; LENGTH: 2072
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: GenBank ID No. US20040010136A1 g178197
US-10-305-720-1181

Query Match          100.0%; Score 21; DB 12; Length 2072;
Best Local Similarity 100.0%; Pred. No. 3.9;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCATCATCCCTTCTCGCT 21
DB 601 GCTCATCATCCCTTCTCGCT 621

RESULT 9
US-10-225-567A-41
; Sequence 41, Application US/10225567A
; Publication No. US20030113798A1
; GENERAL INFORMATION:
; APPLICANT: Lifespan Biosciences
; APPLICANT: Brown, Joseph P.
; APPLICANT: Burnet, Glenn C.
; APPLICANT: Roush, Christine L.
; TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS
; FILE REFERENCE: 1920-4-4
; CURRENT APPLICATION NUMBER: US/10/225,567A
; CURRENT FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 60/257,144
; PRIOR FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 2292
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 41
; LENGTH: 3274
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-225-567A-41

Query Match          100.0%; Score 21; DB 15; Length 3274;
Best Local Similarity 100.0%; Pred. No. 4;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCATCATCCCTTCTCGCT 21
DB 189 GCTCATCATCCCTTCTCGCT 209

RESULT 10
US-10-311-455-48/C
; Sequence 48, Application US/10311455
; Publication No. US20030143606A1
; GENERAL INFORMATION:
; APPLICANT: Olek, Alexander
; APPLICANT: PIEPENBROCK, Christian
; APPLICANT: BERLIN, Kurt
; TITLE OF INVENTION: Diagnosis of Diseases Associated with the Immune System by Determining Cytosine Methylation
; FILE REFERENCE: 5013.1014
; CURRENT APPLICATION NUMBER: US/10/311,455
; CURRENT FILING DATE: 2002-12-16
; PRIOR APPLICATION NUMBER: PCT/EP01/07537
; PRIOR FILING DATE: 2001-07-02
; PRIOR APPLICATION NUMBER: DE 10032529.7
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: DE 10043826.1
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 2424
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SEQ ID NO 48
LENGTH: 6904
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
NAME/KEY: unsure
LOCATION: 821
OTHER INFORMATION: n is a or g or c or t
US-10-311-455-48

Query Match
Best Local Similarity 100.0%; Score 21; DB 13; Length 6904;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCATCATCCCTTCTCGCT 21
DB 1716 GCTCATCATCCCTTCTCGCT 1696

RESULT 11
US-10-001-073-24
Sequence 24, Application US/10001073
Publication No. US20030113725A1
GENERAL INFORMATION:
APPLICANT: Liggett, Stephen
APPLICANT: Small, Kirsten
TITLE OF INVENTION: Alpha-2-adrenergic receptor polymorphisms
FILE REFERENCE: 13073-PCT
CURRENT APPLICATION NUMBER: US/10/001,073
CURRENT FILING DATE: 2001-11-01
NUMBER OF SEQ ID NOS: 53
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 24
LENGTH: 1350
TYPE: DNA
ORGANISM: Homo sapiens
US-10-001-073-24

Query Match
Best Local Similarity 92.4%; Score 19.4; DB 15; Length 1350;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GCTCATCATCCCTTCTCGCT 21
DB 252 GCTCATCATCCCTTCTCGCT 272

RESULT 12
US-10-001-073-25
Sequence 25, Application US/10001073
Publication No. US20030113725A1
GENERAL INFORMATION:
APPLICANT: Liggett, Stephen
APPLICANT: Small, Kirsten
TITLE OF INVENTION: Alpha-2-adrenergic receptor polymorphisms
FILE REFERENCE: 13073-PCT
CURRENT APPLICATION NUMBER: US/10/001,073
CURRENT FILING DATE: 2001-11-01
NUMBER OF SEQ ID NOS: 53
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 25
LENGTH: 1350
TYPE: DNA
ORGANISM: Homo sapiens
US-10-001-073-25

Query Match
Best Local Similarity 92.4%; Score 19.4; DB 15; Length 1350;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GCTCATCATCCCTTCTCGCT 21

DB 252 GCTCATCATCCCTTCTCGCT 272

RESULT 13
US-10-305-720-1180
Sequence 1180, Application US/10305720
Publication No. US20040010136A1
GENERAL INFORMATION:
APPLICANT: Au-Young, Janice K.; Seilhamer, Jeffrey J.
TITLE OF INVENTION: Composition for the Detection of Signaling Pathway Gene Expressio
FILE REFERENCE: PA-0002-1 CON
CURRENT APPLICATION NUMBER: US/10/305,720
CURRENT FILING DATE: 2002-11-26
PRIOR FILING DATE: 1998-01-30
NUMBER OF SEQ ID NOS: 1490
SOFTWARE: PERL Program
SEQ ID NO 1180
LENGTH: 3604
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
OTHER INFORMATION: GenBank ID No. US20040010136A1 G178195
US-10-305-720-1180

Query Match
Best Local Similarity 92.4%; Score 19.4; DB 12; Length 3604;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GCTCATCATCCCTTCTCGCT 21
DB 2329 GCTCATCATCCCTTCTCGCT 2349

RESULT 14
US-10-225-567A-39
Sequence 39, Application US/10225567A
Publication No. US20030113798A1
GENERAL INFORMATION:
APPLICANT: Lifespan Biosciences
APPLICANT: Brown, Joseph P.
APPLICANT: Burner, Glenn C.
APPLICANT: Roush, Christine L.
TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS
FILE REFERENCE: 1920-4-4
CURRENT APPLICATION NUMBER: US/10/225,567A
CURRENT FILING DATE: 2001-12-19
PRIOR APPLICATION NUMBER: 60/257,144
PRIOR FILING DATE: 2000-12-19
NUMBER OF SEQ ID NOS: 2292
SOFTWARE: PatentIn version 3.1
SEQ ID NO 39
LENGTH: 3653
TYPE: DNA
ORGANISM: Homo sapiens
US-10-225-567A-39

Query Match
Best Local Similarity 92.4%; Score 19.4; DB 15; Length 3653;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GCTCATCATCCCTTCTCGCT 21
DB 1131 GCTCATCATCCCTTCTCGCT 1151

RESULT 15
US-10-311-455-46/C
Sequence 46, Application US/10311455
Publication No. US20030143606A1
GENERAL INFORMATION:


```

; APPLICANT: OLEK, Alexander
; APPLICANT: PIEPENBROCK, Christian
; APPLICANT: BERLIN, Kurt
; TITLE OF INVENTION: Diagnosis of Diseases Associated with the Immune System by Determ
; TITLE OF INVENTION: cytosine methylation
; FILE REFERENCE: 5013.1014
; CURRENT APPLICATION NUMBER: US/10/311,455
; CURRENT FILING DATE: 2002-12-16
; PRIOR APPLICATION NUMBER: PCT/EP01/07537
; PRIOR FILING DATE: 2001-07-02
; PRIOR APPLICATION NUMBER: DE 10032529.7
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: DE 10043826.1
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 2424
; SEQ ID NO 46
; LENGTH: 7353
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-311-455-46

Query Match          92.4%; Score 19.4; DB 13; Length 7353;
Best Local Similarity 95.2%; Pred. No. 22;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1  GCTCATCATCCCTTCTCGCT 21
          |||||
Db      2102 GCTCGTCATCCCTTCTCGCT 2082
```

Search completed: February 12, 2004, 06:15:35
Job time : 124.341 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 12, 2004, 03:54:41 ; Search time 1135.79 Seconds
(without alignments)
449.373 Million cell updates/sec

Title: US-09-692-077D-13
Perfect score: 21
Sequence: 1 gctcatcacccttcgcgc 21

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 22781392 seqs, 12152238056 residues
Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
EST:
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_hic:*
9: gb_est1:*
10: gb_est2:*
11: gb_hic:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estcom:*
17: em_gss_hum:*
18: em_gss_hiv:*
19: em_gss_pln:*
20: em_gss_vrt:*
21: em_gss_fun:*
22: em_gss_mam:*
23: em_gss_mus:*
24: em_gss_pro:*
25: em_gss_rtd:*
26: em_gss_phg:*
27: em_gss_vrt1:*
28: gb_gss1:*
29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	19.4	92.4	297	13	BQ302172 QV0-BT026
2	19.4	92.4	2410	11	BC035047 Homo sapi
3	18.4	87.6	619	10	AW916723 ESTJ48027
4	18.4	87.6	658	28	BH735033 BOMDM37TR

5	18.4	87.6	676	28	AQ448022 mgxb0016A
6	18.4	87.6	939	28	BH573939 BOGVT08TR
7	18.4	87.6	809	29	BZ752626 PUDCT72TR
8	18.4	87.6	945	29	BZ752631 PUDCT72TR
9	17.8	84.8	458	29	AJ514080 AJ514080
10	17.8	84.8	505	29	BZ374377
11	17.8	84.8	642	13	B0100970
12	17.8	84.8	650	10	BE427478
13	17.8	84.8	718	13	B0101040
14	17.8	84.8	817	13	A1113972
15	17.8	84.8	971	10	BE420874
16	17.8	84.8	2225	12	BG842980
17	17.4	82.9	260	9	A1978394
18	17.4	82.9	260	9	A1978395
19	17.4	82.9	283	9	AU165754
20	17.4	82.9	287	10	BF763943
21	17.4	82.9	416	12	BT798818
22	17.4	82.9	509	28	AQ879807
23	17.4	82.9	564	12	BT798125
24	17.4	82.9	606	13	BT212727
25	17.4	82.9	665	14	CB664045
26	17.4	82.9	689	28	BH984874
27	17.4	82.9	706	13	BT310902
28	17.4	82.9	736	28	AZ331421
29	17.4	82.9	791	14	CB650823
30	17.4	82.9	811	29	BZ627353
31	17.4	82.9	1369	29	BZ580030
32	16.8	80.0	163	9	AJ503138
33	16.8	80.0	330	10	BB123120
34	16.8	80.0	439	9	AJ502560
35	16.8	80.0	439	9	AJ503843
36	16.8	80.0	442	29	BZ319189
37	16.8	80.0	461	28	AQ864185
38	16.8	80.0	462	28	AQ147051
39	16.8	80.0	464	28	AQ024975
40	16.8	80.0	467	9	A1998046
41	16.8	80.0	518	10	BF016210
42	16.8	80.0	536	13	BQ827804
43	16.8	80.0	559	28	AZ156636
44	16.8	80.0	570	14	CD552619
45	16.8	80.0	593	9	A1728961

ALIGNMENTS

RESULT 1
LOCUS BQ302172 297 bp mRNA linear EST 16-MAY-2002
QV0-BT0263-101299-072-h10 BT0263 Homo sapiens CDNA, mRNA sequence.
ACCESSION BQ302172
VERSION BQ302172.1 GI:20817694

KEYWORDS
SOURCE EST.
ORGANISM Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 297)
Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Britner, M. R.,
Nagai, M. A., da Silva, W. Jr., Zago, M. A., Bordin, S., Costa, F. F.,
Goldman, G. H., Carvalho, A. F., Matsukuma, A., Bala, G. S., Simpson, D. H.,
Brunstein, A., de Oliveira, P. S., Bucher, P., Jongeneel, C. V., O'Hare,
M. J., Soares, P., Brentani, R. K., Reis, L. F., de Souza, S. J. and
Simpson, A. J.

TITLE
Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

JOURNAL
MEDLINE
PUBMED
10737800

COMMENT
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,

Brazil
 Tel: +55-11-2704922
 Fax: +55-11-2707001
 Email: asimpson@ludwig.org.br
 This sequence was derived from the FADES/P/LICR Human Cancer Genome Project. This entry can be seen in the following URL
 (http://www.ludwig.org.br/scripts/gethtml2.pl?cl=QV0&f2=QV0-BT0263-101299-072-h10&f3=1999-12-10&f4=1)
 Seq primer: puc 18 forward
 High quality sequence start: 26
 High quality sequence stop: 205.
 Location/Qualifiers
 1..237
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /dev_stage="Adult"
 /clone_lib="BT0263"
 /note="Organ: Breast; Vector: puc18; Site 1: SmaI; Site 2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196 716 - Ludwig Institute for Cancer Research) profiles into the puc 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

BASE COUNT 40 a 109 c 91 g 57 t
 ORIGIN

Query Match 92.4%; Score 19.4; DB 13; Length 297;
 Best Local Similarity 95.2%; Pred. No. 3.7e+02;
 Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GCTCATCATCCCTTCTCGCT 21
 |||||
 DB 262 GCTCATCATCCCTTCTCGCT 282

RESULT 2 BC035047 2410 bp mRNA linear HTC 23-SEP-2002
 LOCUS HOMO SAPIENS, Similar to adrenergic, alpha-2A-, receptor, clone
 DEFINITION IMAGE:5266354, mRNA.
 ACCESSION BC035047
 VERSION BC035047.1 GI:23272892
 KEYWORDS HTC.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 1 (bases 1 to 2410)
 Strausberg, R.
 Direct Submission
 Submitted (31-JUL-2002) National Institutes of Health, Mammalian
 Gene Collection (MGC), Cancer Genomics Office, National Cancer
 Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
 USA
 NIH-MGC Project URL: http://mgc.nci.nih.gov
 Contact: MGC help desk
 Email: cgabbs-remail.nih.gov
 Tissue Procurement: Miklos Palcovits, M.D., Ph.D.
 CDNA Library Preparation: Michael J. Brownstein (NHGRI) & Shiraki
 Tohyuki and Piero Carninci (RIKEN)
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Institute for Systems Biology
 http://www.systemsbio.org
 contact: amadan@systemsbio.org
 Anup Madan, Jessica Fahey, Erin Helton, Mark Kettelman, Anuradha
 Madan, Stephanie Rodrigues, Amy Sanchez and Michelle Whiting

REMARK
 COMMENT
 Clone distribution: MGC clone distribution information can be found
 through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
 Series: IRAK Place: 73 Row: 0 Column: 16
 This clone was selected for full length sequencing because it

FEATURES
 source
 1..2410
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone_lib="IMAGE:5266354"
 /issue_type="Testis"
 /clone_lib="NIH MGC_97"
 /lab_host="PH10B"
 /note="Vector: pBluescript"

BASE COUNT 406 a 813 c 721 g 470 t
 ORIGIN

Query Match 92.4%; Score 19.4; DB 11; Length 2410;
 Best Local Similarity 95.2%; Pred. No. 8.9e+02;
 Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GCTCATCATCCCTTCTCGCT 21
 |||||
 DB 465 GCTCATCATCCCTTCTCGCT 485

RESULT 3 AW916723 619 bp mRNA linear EST 25-MAY-2000
 LOCUS EST348027 Rat gene index, normalized rat, norvegicus, Bento Soares
 DEFINITION Rattus norvegicus cDNA clone RGID795 5' end, mRNA sequence.
 ACCESSION AW916723
 VERSION AW916723.1 GI:8082456
 KEYWORDS EST.
 SOURCE Rattus norvegicus (Norway rat)
 ORGANISM Rattus norvegicus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
 Rattus.
 1 (bases 1 to 619)
 Lee, N.H., Glodok, A., Chandra, I., Mason, T.M., Quackenbush, J.,
 Kerlavage, A.R., and Adams, M.D.
 Rat Genome Project: Generation of a Rat EST (RESE) Catalog & Rat
 Gene Index
 Unpublished
 Contact: Lee, NH
 The Institute for Genomic Research
 9712, Medical Center Drive, Rockville, MD 20850, USA
 Tel: (301)-838-3529
 Fax: (301)-838-0208
 Email: nhlee@tigr.org
 This clone is available through the ATCC, contact the ATCC
 tel#703-365-2700 for further information
 Seq primer: M13 Reverse
 Location/Qualifiers
 1..619
 /organism="Rattus norvegicus"
 /mol_type="mRNA"
 /db_xref="taxon:10116"
 /clone="RGID795"
 /tissue_type="mix - brain, ovary, placenta, kidney, lung,
 liver, embryo, heart, muscle, spleen"
 /lab_host="SOLR"
 /clone_lib="Rat gene index, normalized rat, norvegicus,
 Bento Soares"
 /note="Vector: pBluescript SK(-); Site 1: EcoRI; Site 2:
 XhoI; Estimated insert size approx.1 kb"

BASE COUNT 105 a 203 c 177 g 134 t
 ORIGIN

Query Match 87.6%; Score 18.4; DB 10; Length 619;
 Best Local Similarity 95.0%; Pred. No. 1.3e+03;
 Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 CTCATCATCCCTTCTCGCT 21

Db 588 CTCATCATCCCTTCTCTCT 607

RESULT 4
LOCUS BH735033/c 658 bp DNA linear GSS 20-FEB-2002

DEFINITION BOMDM37TR BO_2_3 KB Brassica oleracea genomic clone BOMDM37,
genomic survey sequence.

ACCESSION BH735033

VERSION BH735033.1 GI:18840428

KEYWORDS GSS.

SOURCE

ORGANISM

Brassica oleracea
Brassica oleracea
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids
; euroside II; Brassicales; Brassicaceae; Brassica.

REFERENCE 1 (bases 1 to 658)

Town,C.D., Van Aken,S., Uteerback,T., Koo,H. and Fraser,C.M.

Whole genome shotgun sequencing of Brassica oleracea

Unpublished

Other GSSs: BOMDM37TR

Contact: Chris Town

TIGR

9712 Medical Center Drive, Rockville, MD 20850, USA.

Tel: 301-838-3523

Fax: 301-838-0208

Email: cdtown@tigr.org

DNA is from a doubled haploid provided by Tom Osborn.

Seq primer: TR

Class: sheared ends.

Location/Qualifiers

FEATURES

source 1..658
/organism="Brassica oleracea"
/mol_type="genomic DNA"
/strain="T0100DH3"
/db_xref="taxon:3712"
/clone="BOMDM37"
/clone_1b="BO_2_3 KB"
/note="Vector: pHOSt; Site 1: BactI; 2-3 kb sheared
genomic DNA inserted into pHOSt using BactI linkers"

BASE COUNT 211 a 84 c 159 g 204 t

ORIGIN

Query Match 87.6%; Score 18.4; DB 28; Length 658;

Best Local Similarity 95.0%; Pred. No. 1.4e+03;

Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 CTCATCATCCCTTCTCTGCT 21

Db 396 CTCATCATCCCTTCTCTGCT 377

RESULT 5
LOCUS AQ448022 676 bp DNA linear GSS 08-APR-1999

DEFINITION mgxb0016A14f CUGI Rice Blast BAC Library Magnaporthe grisea genomic
clone mgxb0016A14f, genomic survey sequence.

ACCESSION AQ448022

VERSION AQ448022.1 GI:4577159

KEYWORDS GSS.

SOURCE

Magnaporthe grisea (anamorph: Pyricularia grisea)

ORGANISM

Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Sordariomycetes incertae sedis; Magnaportheaceae; Magnaporthe.

REFERENCE 1 (bases 1 to 676)

Yu,Y., Zhu,H., Boyd,C.A., Gaudette,B., Gayle,A., Kingsbury,R.,
Phillips,K., Sasinowski,M., Wing,R.A. and Dean,R.A.

A BAC End Sequencing Framework to Sequence the Magnaporthe grisea

Genome

Unpublished

Contact: Dean RA

Clemson University Genomics Institute

JOURNAL COMMENT

Clemson University
100 Jordan Hall, Clemson University, Clemson, SC 29634
Tel: 864 656 5737
Fax: 864 656 4293
Email: rdean@clemson.edu

Seq primer: TTAATACACTCACTATAGG

Class: BAC ends

High quality sequence start: 37

High quality sequence stop: 300.

Location/Qualifiers

FEATURES

source

1..676
/organism="Magnaporthe grisea"
/mol_type="genomic DNA"
/strain="70-15"
/db_xref="taxon:148305"
/clone="mgxb0016A14f"
/tissue_type="Protoplasts"
/lab_host="E. coli DH10B"
/clone_1b="CUGI Rice Blast BAC Library"
/note="Vector: pBACWICH; Site 1: HindIII; Site 2: HindIII;
Rice blast is one of the most devastating fungal diseases
of rice world wide. It is a filamentous ascomycete with
a haploid genome (n=7) of approximately 40 Mbp. Rice
blast is an important model fungal pathogen for studying
numerous aspects of the fungal-host interaction. In
order to facilitate genome wide analysis, a BAC library
containing 9216 clones with an average insert size of 130
kbp was constructed. This library represents greater
than 25X genome coverage. High density colony filters
are available upon request."

BASE COUNT 115 a 204 c 150 g 206 t 1 others

ORIGIN

Query Match 87.6%; Score 18.4; DB 28; Length 676;

Best Local Similarity 95.0%; Pred. No. 1.4e+03;

Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 CTCATCATCCCTTCTCTGCT 21

Db 632 CTCATCATCCCTTCTCTGCT 651

RESULT 6
LOCUS BH573939 839 bp DNA linear GSS 14-DEC-2001

DEFINITION BOGV08TR BOGV Brassica oleracea genomic clone BOGV08, genomic
survey sequence.

ACCESSION BH573939

VERSION BH573939.1 GI:17825778

KEYWORDS GSS.

SOURCE

ORGANISM

Brassica oleracea

Brassica oleracea
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids
; euroside II; Brassicales; Brassicaceae; Brassica.

REFERENCE 1 (bases 1 to 839)

Town,C.D., Van Aken,S., Uteerback,T., Koo,H. and Fraser,C.M.

Whole genome shotgun sequencing of Brassica oleracea

Unpublished

Other GSSs: BOGV08TR

Contact: Chris Town

TIGR

9712 Medical Center Drive, Rockville, MD 20850, USA.

Tel: 301-838-3523

Fax: 301-838-0208

Email: cdtown@tigr.org

DNA is from a doubled haploid provided by Tom Osborn.

Seq primer: TR

Class: sheared ends.

Location/Qualifiers

FEATURES

source

1..839
/organism="Brassica oleracea"
/mol_type="genomic DNA"

BASE COUNT 274 a 106 c 200 g 259 t
 ORIGIN genomic DNA inserted into pHOSt1 using BstXI linkers"

Query Match 87.6%; Score 18.4; DB 28; Length 839;
 Best Local Similarity 95.0%; Pred. No. 1.5e+03;
 Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Db 2 CTGATCATCCCTTCTCGCT 21
 271 CTGATCATCCCTTCTAGCT 252

RESULT 7
 BZ752626 909 bp DNA linear GSS 10-MAR-2003
 LOCUS PUDCT72TB_ZM_0.6_1.0_KB Zea mays genomic clone ZMMBTA157L24,
 DEFINITION genomic survey sequence.
 ACCESSION BZ752626
 VERSION BZ752626.1 GI:28904975
 KEYWORDS GSS.
 SOURCE Zea mays
 ORGANISM Zea mays
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
 1 (bases 1 to 909)
 White, J.A., Fraser, C.M., Yuan, Y., San Miguel, P., Ma, J. and Bennett, J.
 'A', Fraser, C.M., Yuan, Y., San Miguel, P., Ma, J. and Bennett, J.
 Maize Genomics Consortium
 Unpublished
 Other GSSs: PUDCT72TD
 TIGR
 Contact: Cathy Whitelaw
 9712 Medical Center Drive, Rockville, MD 20850, USA
 Tel: 301-838-5843
 Fax: 301-838-0208
 Email: whitelaw@cigr.org
 Seq primer: TR
 Class: sheared ends.

REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 COMMENT
 BASE COUNT 280 a 178 c 169 g 282 t
 ORIGIN Cot selected genomic DNA library"

FEATURES
 source location/Qualifiers
 1..909
 /organism="Zea mays"
 /mol_type="genomic DNA"
 /strain="B73"
 /db_xref="taxon:4577"
 /clone="ZMMBTA157L24"
 /note="Vector: PCR4-TOPO; Site 1: EcoRI; 0.6-1.0 kb high
 Cot selected genomic DNA library"

Query Match 87.6%; Score 18.4; DB 29; Length 909;
 Best Local Similarity 95.0%; Pred. No. 1.6e+03;
 Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Db 2 CTGATCATCCCTTCTCGCT 21
 533 CTGATCATCCCTTCAAGCT 552

RESULT 8
 BZ752631/c 945 bp DNA linear GSS 10-MAR-2003
 LOCUS PUDCT72TD_ZM_0.6_1.0_KB Zea mays genomic clone ZMMBTA157L24,
 DEFINITION genomic survey sequence.
 ACCESSION BZ752631

VERSION BZ752631.1 GI:28904980
 KEYWORDS GSS.
 SOURCE Zea mays
 ORGANISM Zea mays

REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 COMMENT
 BASE COUNT 295 a 183 c 174 g 293 t
 ORIGIN Cot selected genomic DNA library"

FEATURES
 source location/Qualifiers
 1..945
 /organism="Zea mays"
 /mol_type="genomic DNA"
 /strain="B73"
 /db_xref="taxon:4577"
 /clone="ZMMBTA157L24"
 /note="Vector: PCR4-TOPO; Site 1: EcoRI; 0.6-1.0 kb high
 Cot selected genomic DNA library"

Query Match 87.6%; Score 18.4; DB 29; Length 945;
 Best Local Similarity 95.0%; Pred. No. 1.6e+03;
 Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Db 2 CTGATCATCCCTTCTCGCT 21
 565 CTGATCATCCCTTCAAGCT 546

RESULT 9
 AJ514080/c 458 bp mRNA linear EST 14-NOV-2002
 LOCUS AJ514080 Gossypium hirsutum ovule first day the flower opens
 DEFINITION Gossypium hirsutum cDNA clone su086d07x3, mRNA sequence.
 ACCESSION AJ514080
 VERSION AJ514080.1 GI:24977563
 KEYWORDS EST.
 SOURCE Gossypium hirsutum (upland cotton)
 ORGANISM Gossypium hirsutum

REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 COMMENT
 BASE COUNT 158
 ORIGIN Location/Qualifiers
 1..458
 /organism="Gossypium hirsutum"
 /mol_type="mRNA"
 /cultiivar="Zhongmian12"
 /db_xref="taxon:3635"
 /clone="su086d07x3"
 /tissue_type="ovule"

FEATURES
 source
 The Institute of Genetics and Developmental Biology CAS
 Nanjing 3, Zhongguancun, Haidian, Beijing, 100080, China.

```

/dev_stage="first day the flower opens"
/clone_lib="Gossypium hirsutum ovule first day the flower
opens"
BASE COUNT      180 a      139 c      136 g      3 t
ORIGIN

Query Match      84.8%; Score 17.8; DB 9; Length 458;
Best Local Similarity 90.5%; Pred. No. 2.1e+03;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 GGTGATCATCCCTTCTCGCT 21
Db      26 GGTGATCTTCCCTTCTCTCCT 6

RESULT 10
BZ374377/c      505 bp      DNA      linear      GSS 26-NOV-2002
LOCUS
DEFINITION      1e24c01.g2 WGS-Zmaysf (DH5a methyl filtered) Zea mays genomic clone
ACCESSION      BZ374377
VERSION      BZ374377
KEYWORDS      BZ374377.1 GI:25460894
SOURCE
ORGANISM      Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 505)
Rabinowicz,P.D., O'Shaughnessy,A.L., Ballja,V., Dedhia,N.,
Katzemburger,F., King,L., Miller,B., Muller,S., Naeacimento,L.,
Zutavern,T., McCombie,W.R. and Marijnsen,R.A.
Genomic shotgun sequences from Zea mays (methyl-filtered)
Unpublished
Contact: W. Richard McCombie
Cold Spring Harbor Genome Sequencing Center
Cold Spring Harbor Laboratory
PO Box 100, Cold Spring Harbor, NY 11724, USA
Tel: 516 367 8884
Fax: 516 367 8874
Email: mcombie@cshl.org
Plate: 1e24 row: C Column: 01
Seq primer: -21M13UnivRev
Class: shotgun
High quality sequence stop: 505.
Location/Qualifiers
1.505
/organism="Zea mays"
/mol_type="genomic DNA"
/cultivar="B73"
/db_xref="taxon:4577"
/clone="1e24c01"
/lab_host="DH5a"
/lab_host="WGS-Zmaysf (DH5a methyl filtered)"
/notes="Organ: immature ears; Site 1: Xba I; Site 2: Xba I;
The vector was digested with XbaI and one nucleotide was
added by fill in in the recessive 3' end. The genomic DNA
was nebulized, end repaired, adaptor ligated and size
fractionated using sephadex. The resulting fragments were
between 0.8 and 3 kb and were cloned into the vector (x/y
reads in M13mp19, b/g reads in pUC19). The same ligation
was transformed into DH5a."
BASE COUNT      112 a      146 c      141 g      106 t
ORIGIN

Query Match      84.8%; Score 17.8; DB 29; Length 505;
Best Local Similarity 90.5%; Pred. No. 2.2e+03;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 GGTGATCATCCCTTCTCGCT 21
Db      478 GGTGATCATCCCTTCTCTCT 458

```

```

RESULT 11
BU100970/c      642 bp      mRNA      linear      EST 29-AUG-2002
LOCUS
DEFINITION      WHE3360_A09 A18ZS Chinese Spring aluminum-stressed root tip cDNA
library Triticum aestivum cDNA clone WHE3360_A09_A18, mRNA
sequence.
ACCESSION      BU100970
VERSION      BU100970.1 GI:22548769
KEYWORDS      EST.
SOURCE      Triticum aestivum (bread wheat)
ORGANISM      Triticum aestivum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae
; Triticeae; Triticum.
1 (bases 1 to 642)
Anderson,O.D., Chao,S., Chin,A., Close,T.J., Crossman,C., Gustafson
,J.P., Lazo,G.R., Pham,J., Rauech,C.D., Ross,K., Wilson,C. and Woo
,J.
The structure and function of the expressed portion of the wheat
genomes - Chinese Spring aluminum-stressed root tip cDNA library
Unpublished
Contact: Olin Anderson
US Department of Agriculture, Agriculture Research Service, Pacific
West Area, Western Regional Research Center
800 Buchanan Street, Albany, CA 94710, USA
Tel: 5105595773
Fax: 5105595818
Email: anderson@pw.usda.gov
Sequences have been trimmed to remove vector sequence and low
quality sequence with phred score less than 20
Seq primer: SK primer.
Location/Qualifiers
1.642
/organism="Triticum aestivum"
/mol_type="mRNA"
/cultivar="Chinese Spring"
/db_xref="taxon:4565"
/clone="WHE3360_A09_A18"
/tissue_type="root tip at 1.0 to 1.5 mm stage"
/dev_stage="Seedling"
/lab_host="E. coli SOLR"
/clone_lib="Chinese Spring aluminum-stressed root tip cDNA
library"
/notes="Vector: Lambda uni-ZAP XR, excised phagemid;
Site_1: EcoRI; Site_2: XhoI; Plants were grown for four
days under hydroponic conditions with 1ppm aluminum, root
tips were excised and snap frozen, and total RNA was
prepared at University of Missouri in the JP Gustafson lab
(Ross). Poly(A) RNA was purified, a cDNA library was made,
and the cDNA clones were in vivo excised to give
pBluescript SK(-) phagemids in the TJ Close lab (Chin) at
the University of California, Riverside. Plasmid DNA
preparations and DNA sequencing were performed in the OD
Anderson lab (all other authors)."
BASE COUNT      201 a      124 c      176 g      141 t
ORIGIN

Query Match      84.8%; Score 17.8; DB 13; Length 642;
Best Local Similarity 90.5%; Pred. No. 2.4e+03;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 GGTGATCATCCCTTCTCGCT 21
Db      397 GGTGATCATCCCTTCTCGCT 377

RESULT 12
BE427478/c      650 bp      mRNA      linear      EST 24-JUL-2000
LOCUS
DEFINITION      PSR7068 ITEC PSR Wheat Pericarp/Testa Library Triticum aestivum
cDNA clone PSR7068, mRNA sequence.
ACCESSION      BE427478

```

VERSION BE427478.1 GI:9425321
 KEYWORDS EST.
 SOURCE Triticum aestivum (bread wheat)
 ORGANISM Triticum aestivum
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae
 ; Triticaceae; Triticum.
 1 (bases 1 to 650)
 REFERENCE
 AUTHORS Anderson,O.A., Appels,R., Bailey,P., Blake,T., Close,T., Cloutier
 S., Dubcovsky,J., Feuillet,C., Gale,M., Griner,A., Gustafson,P.,
 Hermann,R.G., Holton,T., Jacquemelin,J.M., Jia,T., Joudrier,P.,
 Langridge,P., Lazo,G.R., Lin,J.J., McGuire,P., Ogihara,Y.,
 Pecchioni,N., Qualset,C., Schuch,W., Selvaraj,G., Shariflou,M.,
 Sorrells,M., Warburton,M. and Wenzel,G.
 International Triticaceae EST Cooperative (ITREC): Production of
 Expressed Sequence Tags for Species of the Triticaceae
 Unpublished (2000)
 JOURNAL
 COMMENT Contact: Bailey P
 Cereals Group, John Innes Centre
 Norfolk, Norwich NR4 7UH UNITED KINGDOM
 Tel: 44 1603 452571 ext. 2387
 Fax: 44 1603 502241
 Email: paul.bailey@bbsrc.ac.uk
 International Triticaceae EST Cooperative (ITREC)
 http://wheat.pw.usda.gov/genome.
 Location/Qualifiers
 1..650
 /organism="Triticum aestivum"
 /mol_type="mRNA"
 /cultivar="Novosibirskaya 67"
 /db_xref="taxon:4565"
 /clone="PSR7068"
 /tissue_type="pericarp/testa"
 /dev_stage="3.1 mix 10:20 days post anthesis"
 /clone_lib="ITREC PSR wheat pericarp/testa library"
 /note="Vector: Lambda ZAP II (Stratagene)"
 BASE COUNT 190 a 122 c 160 g 162 t 16 others
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 Best Local Similarity 90.5%; Pred. No. 2.4e+03;
 Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 GCTCATCATCCCTTTCGGCT 21
 Db 280 GCTCATCATCCCTTTCGGCT 260
 RESULT 13 718 bp mRNA linear EST 29-AUG-2002
 BU101040 WHE3361_A09 B172S Chinese Spring aluminum-stressed root tip cDNA
 LOCUS library Triticum aestivum cDNA clone WHE3361_A09_B17, mRNA
 DEFINITION sequence.
 ACCESSION BU101040
 VERSION BU101040.1 GI:2254839
 KEYWORDS EST.
 SOURCE Triticum aestivum (bread wheat)
 ORGANISM Triticum aestivum
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae
 ; Triticaceae; Triticum.
 1 (bases 1 to 718)
 REFERENCE
 AUTHORS Anderson,O.D., Chao,S., Chin,A., Close,T.J., Crossman,C., Gustafson
 J., J., Lazo,G.R., Pham,J., Rauech,C.J., Rose,K., Wilson,C. and Woo
 J.
 The structure and function of the expressed portion of the wheat
 genomes - Chinese Spring aluminum-stressed root tip cDNA library
 Unpublished
 JOURNAL
 COMMENT Contact: Olin Anderson
 US Department of Agriculture, Agriculture Research Service, Pacific
 West Area, Western Regional Research Center
 800 Buchanan Street, Albany, CA 94710, USA

Tel: 5105595773
 Fax: 5105595818
 Email: candersn@pw.usda.gov
 Sequences have been trimmed to remove vector sequence and low
 quality sequence with phred score less than 20
 Seq primer: SK primer.
 Location/Qualifiers
 1..718
 /organism="Triticum aestivum"
 /mol_type="mRNA"
 /cultivar="Chinese Spring"
 /db_xref="taxon:4565"
 /clone="WHE3361_A09_B17"
 /tissue_type="Root tip at 1.0 to 1.5 mm stage"
 /dev_stage="Seedling"
 /lab_host="E. coli SOLR"
 /clone_lib="Chinese Spring aluminum-stressed root tip cDNA
 library"
 /note="Vector: Lambda Uni-ZAP XR, excised phagemid;
 Site 1: EcoRI; Site 2: XhoI; Plants were grown for four
 days under hydroponic conditions with 1ppm aluminum, root
 tips were excised and snap frozen, and total RNA was
 prepared at University of Missouri in the JP Gustafson lab
 (Rose). Poly(A) RNA was purified, a cDNA library was made,
 and the cDNA clones were in vivo excised to give
 Bluescript SK(-) phagemids in the TU Close lab (Chin) at
 the University of California, Riverside. Plasmid DNA
 preparations and DNA sequencing were performed in the OD
 Anderson lab (all other authors)."
 BASE COUNT 222 a 138 c 196 g 162 t
 ORIGIN
 Query Match 84.8% Score 17.8; DB 13; Length 718;
 Best Local Similarity 90.5%; Pred. No. 2.5e+03;
 Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 GCTCATCATCCCTTTCGGCT 21
 Db 397 GCTCATCATCCCTTTCGGCT 377
 RESULT 14 817 bp mRNA linear EST 23-APR-2001
 A1113972 GH10539_Sprime GH Drosophila melanogaster head POT2 Drosophila
 LOCUS melanogaster cDNA clone GH10539.5 similar to CG12781: FBan012781
 DEFINITION located on: 2R 59B4-59B4.1: 04/10/2001, mRNA sequence.
 ACCESSION A1113972
 VERSION A1113972.2 GI:13757849
 KEYWORDS EST.
 SOURCE Drosophila melanogaster (fruit fly)
 ORGANISM Drosophila melanogaster
 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 Ephydroidea; Drosophilidae; Drosophila.
 1 (bases 1 to 817)
 REFERENCE
 AUTHORS Harvey,D., Brokstein,P., Hong,L., Evans-Holm,M., Su,C., Tsang,G.,
 Lewis,S. and Rubin,G.M.
 BDGP/HMMI Drosophila EST Project
 JOURNAL
 COMMENT Unpublished
 On Sep 2, 1998 this sequence version replaced gi:3514775.
 Other_ESTs: GH10539.3prime
 Contact: Stapleton, M.
 BDGP
 Lawrence Berkeley National Lab
 One Cyclotron Rd, Berkeley, CA 94720, USA
 Fax: 510 486 6798
 Email: http://www.fruitfly.org/EST, est@fruitfly.berkeley.edu
 hit genomic AB003459; arm:2R (17805870,18105620)
 estimated-cyto:59B2-59D2: 04/10/2001
 Plate: GH.105 row: D Column: 3
 High quality sequence stop: 579
 POLYA=NO.

FEATURES

source

Location/Qualifiers
 1. 817
 /organism="Drosophila melanogaster"
 /mol_type="mRNA"
 /db_xref="taxon:7227"
 /clone="GH10539"
 /sex="male and female"
 /dev_stage="adult"
 /lab_host="DHS - alpha"
 /clone_lib="GH Drosophila melanogaster head POT2"
 /note="Organ: head; Vector: POT2; Site 1: EcoRI; Site 2: XhoI; Sized fractionated cDNAs were directly ligated into POT2. Plasmid cDNA library."
 BASE COUNT 156 a 213 c 219 g 229 t
 ORIGIN

Query Match 84.8%; Score 17.8; DB 9; Length 817;
 Best Local Similarity 90.5%; Pred. No. 2.7e+03;
 Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 GGTGATCATCCCTTCTCGCT 21
 |||||
 Db 407 GGTCTCTCTCTCTCTCGCT 427

RESULT 15

BE420874

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

JOURNAL

COMMENT

TITLE

FEATURES

source

BE420874 971 bp mRNA linear EST 24-JUL-2000
 HMW003.D11 ITBC HMM Barley Leaf Library Hordeum vulgare subsp.
 BE420874
 BE420874.1 GI:9418717
 EST.
 Hordeum vulgare subsp. vulgare
 Hordeum vulgare subsp. vulgare
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae
 ; Triticeae; Hordeum.
 1 (bases 1 to 971)
 Anderson,O.A., Appels,R., Bailey,P., Blake,T., Close,T., Cloutier
 ,S., Dubcovsky,J., Feuillet,C., Gale,M., Graner,A., Gustafson,P.,
 Hermann,R.G., Holton,T., Jacquemin,J.M., Jia,J., Joudrier,P.,
 Langridge,P., Lazo,G.R., Lin,J.J., McGuire,P., Ogihara,Y.,
 Pecchioni,N., Quiset,C., Schuch,W., Selvaraj,G., Shariflou,M.,
 Sorrells,M., Warburton,M. and Wenzel,G.
 International Triticeae EST Cooperative (ITEC): Production of
 Expressed Sequence Tags for Species of the Triticeae
 Unpublished (2000)
 Contact: Herrmann RG
 Botanisches Institut der LMU
 Menzinger Str. 67, D-80638 Muenchen GERMANY
 Fax: 49 30 171683
 Email: herrmann@botanik.biologie.uni-muenchen.de
 International Triticeae EST Cooperative (ITEC)
 http://wheat.pw.usda.gov/genome.
 Location/Qualifiers
 1. 971
 /organism="Hordeum vulgare subsp. vulgare"
 /mol_type="mRNA"
 /cultivar="Daike"
 /db_xref="taxon:112509"
 /clone="HMW003.D11"
 /issue_type="leaf"
 /dev_stage="14 day old"
 /clone_lib="ITBC HMM Barley Leaf Library"
 /note="Vector: pBluescriptSK(-); 850 bp average insert
 size."
 BASE COUNT 206 a 312 c 145 g 308 t
 ORIGIN

Query Match 84.8%; Score 17.8; DB 10; Length 971;
 Best Local Similarity 90.5%; Pred. No. 2.9e+03;
 Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 GGTGATCATCCCTTCTCGCT 21
 |||||
 Db 825 GGTGATCATCTCTCTCGCT 845

Search completed: February 12, 2004, 06:05:45
 Job time : 1147.79 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using SW model

Run on: February 12, 2004, 01:54:29 ; Search time 615.146 Seconds
(without alignments)
1396.582 Million cell updates/sec

Title: US-09-692-077D-14

Perfect score: 21
Sequence: 1 aaagccacacatgctcgggt 21

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2888711 seqs, 2045481386 residues

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :
1: gb_ba:*
2: gb_hcg:*
3: gb_in:*
4: gb_em:*
5: gb_ov:*
6: gb_pac:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vl:*
15: em_ba:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
20: em_om:*
21: em_or:*
22: em_ov:*
23: em_pac:*
24: em_ph:*
25: em_pl:*
26: em_ro:*
27: em_sts:*
28: em_un:*
29: em_vl:*
30: em_hcg_hum:*
31: em_hcg_inv:*
32: em_hcg_other:*
33: em_hcg_mus:*
34: em_hcg_pia:*
35: em_hcg_rtd:*
36: em_hcg_man:*
37: em_hcg_vtc:*
38: em_hcg_hum:*
39: em_hcg_mus:*
40: em_hcg_mus:*
41: em_hcg_other:*

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	21	100.0	21	AX350502	AX350502 Sequence
2	21	100.0	828	567316	567316 alpha 2-adr
3	21	100.0	885	HUMA2C2	M38742 Human alpha
4	21	100.0	1030	HSNA325747	AJ325747 Homo sapi
5	21	100.0	1344	AX350490	AX350490 Sequence
6	21	100.0	1344	AF316895	AF316895 Homo sapi
7	21	100.0	1353	AX350489	AX350489 Sequence
8	21	100.0	2072	AR270618	AR270618 Sequence
9	21	100.0	2072	HUMADRA2RA	M34041 Human alpha
10	21	100.0	3274	AX548756	AX548756 Sequence
11	21	100.0	9842	AF005590	AF005590 Homo sapi
12	21	100.0	22842	AC092603	AC092603 Homo sapi
13	17.8	84.8	81920	AC019708	AC019708 Drosophill
14	17.8	84.8	153648	AC008210	AC008210 Drosophill
15	17.8	84.8	181905	AC008211	AC008211 Drosophill
16	17.8	84.8	213688	AE003755	AE003755 Drosophill
17	17.8	84.8	259219	AC106994	AC106994 Rattus no
18	17.8	84.8	283336	AC097749	AC097749 Rattus no
19	17.4	82.9	18496	AE001925	AE001925 Deinococc
20	17.4	82.9	201844	CNS05TCL	AL355102 Human chr
21	17	81.0	8607	AE013182	AE013182 Thermoana
22	17	81.0	178967	AC128772	AC128772 Rattus no
23	17	81.0	275605	AC123100	AC123100 Rattus no
24	16.8	80.0	636	CNS01COS	AL114932 Botrytis
25	16.8	80.0	660	CNS01AX1	AL11501 Botrytis
26	16.8	80.0	4313	AB020667	AB020667 Homo sapi
27	16.8	80.0	68040	AC101898	AC101898 Mus muscu
28	16.8	80.0	88883	AC107911	AC107911 Homo sapi
29	16.8	80.0	91966	AC138708	AC138708 Homo sapi
30	16.8	80.0	104435	AC016292	AC016292 Homo sapi
31	16.8	80.0	107529	AC069085	AC069085 Homo sapi
32	16.8	80.0	107529	AC069085	AC069085 Homo sapi
33	16.8	80.0	110865	AY129338	AY129338 Mycobacte
34	16.8	80.0	114800	AC123567	AC123567 Homo sapi
35	16.8	80.0	125856	HS1187M17	AP005884 Oryza sat
36	16.8	80.0	154961	AP005884	AP005884 Human DNA
37	16.8	80.0	157722	AL953890	AL953890 Mouse DNA
38	16.8	80.0	162808	AC021340	AC021340 Homo sapi
39	16.8	80.0	172945	AC108099	AC108099 Homo sapi
40	16.8	80.0	174099	AP005789	AP005789 Oryza sat
41	16.8	80.0	176843	AC026655	AC026655 Homo sapi
42	16.8	80.0	193641	AC121972	AC121972 Mus muscu
43	16.8	80.0	207461	AC111108	AC111108 Mus muscu
44	16.8	80.0	207661	AC015884	AC015884 Homo sapi
45	16.8	80.0	238129	AC094595	AC094595 Rattus no

ALIGNMENTS

RESULT 1
LOCUS AX350502 21 bp DNA
DEFINITION Sequence 14 from Patent WO0179561.
ACCESSION AX350502
VERSION AX350502.1 GI:18616098
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
1 Liggett, S.B. and Small, K.M.
AUTHORS
TITLE Alpha-2 adrenergic receptor polymorphisms
JOURNAL Patent: WO 0179561-A 14 25-OCT-2001;

Pred. No. is the number of results predicted by chance to have a

Ligett, Stephen B. (US) ; Small, Kersten M. (US)
 Location/Qualifiers
 1. 21
 /organism="Homo sapiens"
 /mol_type="genomic DNA"
 /db_xref="taxon:9606"

BASE COUNT 5 a 7 c 6 g 3 t

Query Match 100.0%; Score 21; DB 6; Length 21;
 Best Local Similarity 100.0%; Pred. No. 24;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAAGCCCCACCATGTCGGGT 21
 Db 1 AAAGCCCCACCATGTCGGGT 21

RESULT 2
 567316/c
 LOCUS
 DEFINITION
 alpha-2-adrenergic receptor [rats, Sprague-Dawley, islets of
 Langerhans, mRNA Partial, 828 nt].
 567316
 567316.1 GI:456949

ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM

Rattus sp.
 Rattus sp.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
 Rattus.
 1 (bases 1 to 828)
 Wang, S.Y. and Pilkey, D.T.
 Identification in islets of Langerhans of a new rat alpha
 2-adrenergic receptor
 Diabetes 43 (1), 127-136 (1994)
 JOURNAL
 MEDLINE
 PUBMED
 94085695
 8262309

REMARK
 GenBank staff at the National Library of Medicine created this
 entry [NCBI gisbseq 140730] from the original journal article.
 This sequence comes from Fig. 1.
 Location/Qualifiers
 1. 828
 /organism="Rattus sp."
 /mol_type="mRNA"
 /db_xref="taxon:10118"
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 /note="This sequence comes from Fig. 1"
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 /protein_id="A014006.1"
 /db_xref="GI:30027780"
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 AAVISLPLIYKGDGPOPRGPOCKINOEWYILASISGFPAPCLIMILIVYRIYL
 IAKRSNRGRPAKGRQGSQKOPRPHGALASAKIPALASVASAREVNSHSGTG
 KEKRGTEPDTGTRALPPSWALPNSGQKQGVGASPEDAEAESEEESECEPQAVP
 VSPASACSPPLQOPQGSRLVATLRGVLLGRGVAIGQWRRRAQLTRERKFTFVLA
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BASE COUNT 148 a 271 c 269 g 140 t

ORIGIN

Query Match 100.0%; Score 21; DB 10; Length 828;
 Best Local Similarity 100.0%; Pred. No. 15;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAAGCCCCACCATGTCGGGT 21
 Db 401 AAAGCCCCACCATGTCGGGT 381

RESULT 3
 HUMA2C2/c
 LOCUS
 HUMA2C2 885 bp DNA linear PRI 06-MAR-1995

DEFINITION
 Human alpha-2 adrenergic receptor (ADRA2C) gene, partial cds.
 M38742
 M38742.1 GI:177867
 VERSION
 alpha-2 adrenergic receptor.
 KEYWORDS
 Homo sapiens (human)
 SOURCE
 Homo sapiens
 ORGANISM
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 885)
 Chang, A.C., Ho, T.F. and Chang, N.C.
 In vitro amplification by polymerase chain reaction of a partial
 gene encoding the third subtype of alpha-2 adrenergic receptor in
 humans
 JOURNAL
 Biochem. Biophys. Res. Commun. 172 (2), 817-823 (1990)
 MEDLINE
 PUBMED
 91054503
 2173582

COMMENT
 Original source text: Human adult neuroblastoma DNA, clone PCRA2.
 Draft entry and computer-readable sequence for [unpublished (1990)]
 kindly submitted
 by A.C.Chang, 20-SEP-1990.
 Institute of Neuroscience
 155, Sect II, Li-Noon St.
 Taipei, Taiwan, 11221 ROC.
 Location/Qualifiers
 1. 885
 /organism="Homo sapiens"
 /mol_type="genomic DNA"
 /db_xref="taxon:9606"
 /map="4p16.3-p15"
 /clone="PCRA2"
 /cell_line="neuroblastoma SK-N-SH"
 /cell_type="neuroblastoma"
 /tissue_type="neural"
 /dev_stage="adult"
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 /gene="ADRA2C"
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 /partial
 /gene="ADRA2C"
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 /product="alpha-2-adrenergic receptor"
 /protein_id="AA62823.1"
 /db_xref="GI:177868"
 /db_xref="GDB:G00-120-540"
 /translation="FCTSSIVHLCAISIDRYWAVSRALVNSKRTPRRIKIIITVWLI
 IAAVISLPLIYKGDGPOPRGPOCKINOEWYILASISGFPAPCLIMILIVYRIYL
 IAKRSNRGRPAKGRQGSQKOPRPHGALASAKIPALASVASAREVNSHSGTG
 KEKRGTEPDTGTRALPPSWALPNSGQKQGVGASPEDAEAESEEESECEPQAVP
 QAVPSPASACSPPLQOPQGSRLVATLRGVLLGRGVAIGQWRRRAQLTRERKFT
 FVLAVIVGVLCMPFPFF"

BASE COUNT 152 a 285 c 285 g 163 t

ORIGIN

Query Match 100.0%; Score 21; DB 9; Length 885;
 Best Local Similarity 100.0%; Pred. No. 15;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAAGCCCCACCATGTCGGGT 21
 Db 404 AAAGCCCCACCATGTCGGGT 384

RESULT 4
 HSA325747
 LOCUS
 HSA325747 1030 bp DNA linear PRI 18-JUL-2002
 DEFINITION
 Homo sapiens genomic sequence surrounding Noci site, clone
 NBI-818S.
 AJ325747
 AJ325747.1 GI:15870141

ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM

Homo sapiens (human)
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 1030)
 Kuteenko, A.S., Glatzullin, R.Z., Al-Amin, A.N., Wang, F., Kvashe, S.M.,
 Podowski, R.M., Matushkin, Y.G., Gnanachandani, A., Muravenko, O.V.,
 Levitsky, V.G., Kolchanov, N.A., Protodopov, A.I., Kashuba, V.I.,
 Kiselev, L.L., Maestman, W., Mahlestedt, C., and Zabarovsky, E.R.
 North flanking sequences: a tool for gene discovery and verification
 of the human genome
 Nucleic Acids Res. 30 (14), 3163-3170 (2002)

JOURNAL MEDLINE
 22131767
 12136098
 2 (bases 1 to 1030)
 Zabarovsky, E.R.
 Direct Submission
 Submitted (16-MAY-2001) Microbiology and Tumorbiology Centre,
 Karolinska Institute, Theorells vag, 3, Box 280, Stockholm 171 77,
 Sweden

FEATURES
 source location/Qualifiers
 1..1030
 /organism="Homo sapiens"
 /mol_type="genomic DNA"
 /db_xref="taxon:9606"
 /clone="NBL-818S"

BASE COUNT 211 a 329 c 308 g 182 t

ORIGIN

Query Match 100.0%; Score 21; DB 9; Length 1030;
 Best Local Similarity 100.0%; Pred. No. 15;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAAGCCCAACATGTCGGGT 21
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 393 AAAGCCCAACATGTCGGGT 413

Db

RESULT 5
 AX350490/c 1344 bp DNA linear PAT 06-FEB-2002
 LOCUS Sequence 2 from Patent WO0179561.
 ACCESSION AX350490
 VERSION AX350490.1 GI:18616092
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
 1 Liggett, S.B. and Small, K.M.
 Alpha-2 adrenergic receptor polymorphisms
 Patent: WO 0179561-A 2 25-OCT-2001;
 Liggett, Stephen B. (US); Small, Kersten M. (US)
 Location/Qualifiers
 1..1344
 /organism="Homo sapiens"
 /mol_type="genomic DNA"
 /db_xref="taxon:9606"

BASE COUNT 220 a 458 c 400 g 266 t

ORIGIN

Query Match 100.0%; Score 21; DB 6; Length 1344;
 Best Local Similarity 100.0%; Pred. No. 14;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAAGCCCAACATGTCGGGT 21
 |||||
 686 AAAGCCCAACATGTCGGGT 666

Db

RESULT 6
 AF316895/c 1344 bp DNA linear PRI 13-FEB-2001
 LOCUS Homo sapiens alpha 2B adrenergic receptor (ADRA2B) gene, complete
 cds.

ACCESSION AF316895
 VERSION AF316895.1 GI:12698669
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
 1 (bases 1 to 1344)
 Small, K.M., Brown, K.M., Forbes, S.L., and Liggett, S.B.
 Polymorphic deletion of three intracellular acidic residues of the
 alpha 2B-adrenergic receptor decreases G protein-coupled receptor
 kinase-mediated phosphorylation and desensitization
 J. Biol. Chem. 276 (7), 4917-4922 (2001)

JOURNAL MEDLINE
 21265012
 11056163
 2 (bases 1 to 1344)
 Small, K.M., Brown, K.M., Forbes, S.L., and Liggett, S.B.
 Direct Submission
 Submitted (26-OCT-2000) Internal Medicine, University of
 Cincinnati, 231 Bethesda Ave, Cincinnati, OH 45267, USA

FEATURES
 source location/Qualifiers
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 /product="alpha 2B adrenergic receptor"
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 /note="G-protein coupled receptor"
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 /protein_id="AAK01635.1"
 /db_xref="GI:12698670"
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 APONLFLVSLAADIIVATLIPSLANELLGYWFRRTWCERYIALDVLPCTSSIVH
 LCATSLDRYVAVSRALRYNSKTPRIRICITITWVLAIVSLPLIKGDPQPRG
 RPOCLNDREAWYTLASISIGSFAPCLIMILVLRILYLAISNRGPRPAKGGPGGES
 KOPRSDGGKALASAKLPAALASVARSVNGSKSTGEKEGETPEDTGRLAPSMVA
 LNSGGGAGKEVCGASPPDAEVEEERECECPQAPVPSASCSGPIQDGGGVLA
 TLRGVILGRVGAIGCGWMRRRATLTREKRTFVLAVVIGFVLCWPFPPFSYSLGA
 ICPKCKVPHGLPFFFMIGYCNSSLNPVITYTFNQDFRFRRLICRPWTOTAW"

variation
 891 892
 /gene="ADRA2B"
 /note="compared to wild type sequence presented in GenBank
 Accession Number AF005900; polymorphic sequence lacks
 three glu residues at this location"
 /frequency="Caucasians 0.31; African-Americans 0.12"
 /replace="gaagagagag"

BASE COUNT 220 a 458 c 400 g 266 t

ORIGIN

Query Match 100.0%; Score 21; DB 9; Length 1344;
 Best Local Similarity 100.0%; Pred. No. 14;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAAGCCCAACATGTCGGGT 21
 |||||
 686 AAAGCCCAACATGTCGGGT 666

Db

RESULT 7
 AX350489/c 1353 bp DNA linear PAT 06-FEB-2002
 LOCUS Sequence 1 from Patent WO0179561.
 DEFINITION AX350489
 ACCESSION AX350489
 VERSION AX350489.1 GI:18616091
 KEYWORDS
 SOURCE Homo sapiens (human)

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1
Liggett, S.B. and Small, K.M.
Alpha-2 adrenergic receptor polymorphisms
Patent: WO 0179561-A 1 25-OCT-2001;
JOURNAL Liggett, Stephen B. (US) ; Small, Kersten M. (US)
Location/Qualifiers

FEATURES
source
1..1353
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"

BASE COUNT 224 a 458 c 405 g 266 t

ORIGIN

Query Match 100.0%; Score 21; DB 6; Length 1353;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAAGCCCAACATGTCGGGT 21
|||||
686 AAAGCCCAACATGTCGGGT 666

RESULT 8
AR270618/c 2072 bp DNA linear PAT 10-APR-2003
LOCUS AR270618
DEFINITION Sequence 1181 from patent US 6500938.
ACCESSION AR270618
VERSION AR270618.1 GI:29701852
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 2072)
AUTHORS Au-Young, J. and Seilhamer, J. J.
TITLE Composition for the detection of signaling pathway gene expression
JOURNAL Patent: US 6500938-A 1181 31-DEC-2002;
FEATURES
source
1..2072
/organism="unknown"

BASE COUNT 316 a 705 c 660 g 391 t

ORIGIN

Query Match 100.0%; Score 21; DB 6; Length 2072;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAAGCCCAACATGTCGGGT 21
|||||
1098 AAAGCCCAACATGTCGGGT 1078

RESULT 9
HUMADRA2RA/c 2072 bp DNA linear PRI 30-OCT-1994
LOCUS HUMADRA2RA
DEFINITION Human alpha-2-adrenergic receptor (alpha-2 c2) gene, complete cds.
ACCESSION M34041.1
VERSION M34041.1 GI:118197
KEYWORDS alpha-2-adrenergic receptor; plasma membrane protein; receptor-coupled G protein.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 2072)
AUTHORS Lomasney, J.W., Lorenz, W., Allen, L.F., King, K., Regan, J.W., Yang-Feng, T.L., Caron, M.G. and Lefkowitz, R.J.
TITLE Expansion of the alpha 2-adrenergic receptor family: cloning and characterization of a human alpha 2-adrenergic receptor subtype, the gene for which is located on chromosome 2
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 87 (13), 5094-5098 (1990)

MEDLINE 90311349
PUBMED 2164221
COMMENT Original source text: Human placenta DNA, clone alpha-2 C2. Draft entry and computer-readable sequence for [1] kindly submitted by J.W.Lomasney, 03-MAY-1990, for release after publication.

FEATURES
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/mol_type="genomic DNA"
/db_xref="taxon:9606"

gene
413..1765
/gene="ADRA2B"

CDS
413..1765
/gene="ADRA2B"
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name "ADRA2BL1"

/codon_start=1
/protein_id="AA051666.1"
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APQNLFIYSIAADIVATLIPSLANELGWYERRTCVVALDVLFTSSIV
LCAISLDIRWAVSRALRYNSKTRPRKICITLITWLIANAIVSLPRLIYKGGQDQRC
RPQKRLNCEAWYITLASSIGSFAPCLMIVLRLIYLIAKSNRGPRAKGGQGES
KQPRDHGGLASAKLPALASVASAREVNGHSGTGEKEGETPDGTALPQSWAA
LPSGCGQKEGCGASPEDEAESEEESECEPOAVPVSPASCSPLPOQGS
VLATRGQVILGRGVAIGGOWRRARAHVTRKRTFVLAVIGVFLCWPFFESYS
LCAITPKHCKVHGLFQFFFWIGYCNSSLNPYITIFNDPRARPRILCRPMTQAW
"

BASE COUNT 316 a 705 c 660 g 391 t

ORIGIN Chromosome 2.

Query Match 100.0%; Score 21; DB 9; Length 2072;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAAGCCCAACATGTCGGGT 21
|||||
1098 AAAGCCCAACATGTCGGGT 1078

RESULT 10
AX548756/c 3274 bp DNA linear PAT 26-NOV-2002
LOCUS AX548756
DEFINITION Sequence 41 from Patent WO02061087.
ACCESSION AX548756
VERSION AX548756.1 GI:25813586
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1
AUTHORS Burnier, G.C., Roush, C.L. and Brown, J.P.
TITLE Antigenic peptides, such as for G protein-coupled receptors (GPCRs), antibodies thereto, and systems for identifying such antigenic peptides
JOURNAL Patent: WO 02061087-A 41 08-AUG-2002;
Lifespan Biosciences, Inc. (US)
Location/Qualifiers

FEATURES
source
1..3274
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"

BASE COUNT 587 a 979 c 967 g 741 t

ORIGIN

Query Match 100.0%; Score 21; DB 6; Length 3274;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAAGCCCAACATGTCGGGT 21

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Db      686  AAAAGCCCACTGTCGGGT 666

RESULT 11
AF005900/c 9842 bp DNA linear PRI 08-JUL-1997
LOCUS      Homo sapiens alpha2B-adrenergic receptor (alpha2C2AR) gene,
DEFINITION complete cds.
ACCESSION  AF005900
VERSION     AF005900.1 GI:2245627
KEYWORDS
SOURCE      Homo sapiens (human)
ORGANISM    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 9842)
AUTHORS     Cayla, C., Schack, S., Bouloumie, A., Dovedjian, J. C. and Paris, H.
TITLE       Alpha2C2-adrenergic receptor gene
JOURNAL     Unpublished
REFERENCE   2 (bases 1 to 9842)
AUTHORS     Cayla, C., Schack, S., Bouloumie, A., Dovedjian, J. C. and Paris, H.
TITLE       Direct Submission
JOURNAL     Submitted (29-MAY-1997) INSEEM Unit 317, Institut Louis Bugnard,
            CHU Rangueil, Toulouse 31403, France
FEATURES
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            /mol_type="genomic DNA"
            /db_xref="taxon:9606"
            /chromosome="2"
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            /gene="alpha2C2AR"
            /note="alpha2C2 adrenergic receptor gene"
            /gene="alpha2C2AR"
            /note="adrenergic receptor"
            /codon_start=1
            /product="alpha2B-adrenergic receptor"
            /protein_id="AAB62558.1"
            /db_xref="GI:2245628"
            /translation="MDHDPYSVQATAAIAAIFLLFTFGNALVILAVLSRLR
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            /LCATSLDHYMAVRALEYSKRTPRKICITLWLIAAVISLPLIYKGDGPPRG
            /RQPRDHGALASATLPAALASVAARVNGHSGTGEKEGEPDGTFRALPQPMWA
            /LPNSQDQKGEVGCASPEDEAESEEESEEECECPQAVPASPACSPFLQPCGSR
            /VLATRGQVLLRGVGAIGQWRRRAQLTREKRTFVLAVVIGVFCVCFPFPSYS
            /IGATCPKIKVPHGLPFFFWICGNCSSINPIYITIFNDPFRARRILCRWQTAW
            "

gene
CDS
polyA_signal 8649..8654
BASE COUNT 1870 a 2747 c 3225 g 1998 t 2 others
ORIGIN
Query Match 100.0%; Score 21; DB 9; Length 9842;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  AAAAGCCCACTGTCGGGT 21
DB      6083  AAAAGCCCACTGTCGGGT 6063

RESULT 12
AC092603 22842 bp DNA linear PRI 01-MAR-2002
LOCUS      Homo sapiens BAC clone RP11-13906 from 2, complete sequence.
DEFINITION AC092603 AC073396
ACCESSION  AC092603.2 GI:16303539
VERSION     HTG.
KEYWORDS
SOURCE      Homo sapiens (human)
ORGANISM

```

```

REFERENCE   1 (bases 1 to 22842)
AUTHORS     Sulston, J. E. and Waterston, R.
TITLE       Toward a complete human genome sequence
JOURNAL     Genome Res. 8 (11), 1097-1108 (1998)
MEDLINE     99063792
PUBMED      9847074
REFERENCE   2 (bases 1 to 22842)
AUTHORS     Martinka, S., Abbott, A., Hawkins, M., Elliott, G. and Doeber, A.
TITLE       The sequence of Homo sapiens BAC clone RP11-13906
JOURNAL     Unpublished (2001)
REFERENCE   3 (bases 1 to 22842)
AUTHORS     Waterston, R. H.
TITLE       Direct Submission
JOURNAL     Submitted (19-JUL-2001) Genome Sequencing Center, Washington
            University School of Medicine, 4444 Forest Park Parkway, St. Louis,
            MO 63108, USA
REFERENCE   4 (bases 1 to 22842)
AUTHORS     Waterston, R. H.
TITLE       Direct Submission
JOURNAL     Submitted (20-OCT-2001) Genome Sequencing Center, Washington
            University School of Medicine, 4444 Forest Park Parkway, St. Louis,
            MO 63108, USA
REFERENCE   5 (bases 1 to 22842)
AUTHORS     Waterston, R. H.
TITLE       Direct Submission
JOURNAL     Submitted (23-OCT-2001) Genome Sequencing Center, Washington
            University School of Medicine, 4444 Forest Park Parkway, St. Louis,
            MO 63108, USA
REFERENCE   6 (bases 1 to 22842)
AUTHORS     Waterston, R.
TITLE       Direct Submission
JOURNAL     Submitted (01-MAR-2002) Department of Genetics, Washington
            University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
            On Oct 20, 2001 this sequence version replaced gi:14916188.
COMMENT     ----- Genome Center
            Center: Washington University Genome Sequencing Center
            Center code: WUGSC
            Web site: http://genome.wustl.edu/gsc
            Contact: sapiens@wustl.wustl.edu
            ----- Summary Statistics
            Center project name: H_NH013906
            Drafting Center: WIBR
            -----

```

NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.

This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.

MAPPING INFORMATION: Mapping information for this clone was provided by Dr. John D. McPherson, Department of Genetics, Washington University, St. Louis MO. For additional information about the map position of this sequence, see <http://genome.wustl.edu/gsc>

SOURCE INFORMATION: The RP11-11 human BAC library was made from the blood of one male donor, as described by Osoegawa, K., Woon, P. Y., Zhao, B., Prengen, E., Tateo, M., Cacanese, J. J., and de Jong, P. J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. *Genomics* 51:1-8. The clone may be obtained either from Research Genetics, Inc. (<http://www.resgen.com>) or Pieter de Jong and coworkers at <http://www.chori.org>

VECTOR: pBAC3.6

NEIGHBORING SEQUENCE INFORMATION:

The clone sequenced to the left is RP11-401C13, 2000 bp overlap;
The clone sequenced to the right is RP11-574017, 2000 bp overlap.
Actual end of this clone is at base position 48999 of RP11-574017.

Polymorphisms have been identified between AC013272 and AC092603.

The sequence of AC073396 has been incorporated into AC092603.

FEATURES

source
1. 22842
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="2"
/map="2"
/clone="RP11-139J6"
/clone_1b="RPC1-11"
352..465
/rpt_family="MIR"
1377..1424
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1424..1449
/rpt_family="(GA)n"
1495..1665
/rpt_family="Alu"
1669..1966
/rpt_family="Alu"
2812..2918
/rpt_family="MIR"
3183..3448
/rpt_family="CT-rich"
5541..5566
/rpt_family="AT-rich"
5576..5870
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6195..6301
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6627..6733
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7278..7415
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7688..7723
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8140..8218
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8863..8922
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10172..10296
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10436..10550
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11617..11882
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12062..12532
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12062..12257
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12378..12902
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14413..14439
/rpt_family="(TCC)n"
14762..14832
/note="similar to Homo sapiens EST AL544609 (NID:g12877089) "
misc_feature
14849..16413
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misc_feature
15084..15487
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misc_feature
15110..15648
/note="similar to Rattus norvegicus EST AW916723 (NID:g8082456) "
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18481..18596
/rpt_family="L2"
19265..19675
/rpt_family="L2"
20027..20223
/rpt_family="MER1_type"
20316..20416
/rpt_family="L2"
20537..20973
/rpt_family="L2"
22057..22471
/note="match to EST AA830781 (NID:g2903880) cc56b01.s1"
22057..22208
/note="match to EST AA836522 (NID:g2910841) cd22d08.s1"
BASE COUNT 4797 a 7173 c 6248 g 4624 t
ORIGIN
Query Match 100.0%; Score 21; DB 9; Length 22842;
Best Local Similarity 100.0%; Pred. No. 9.9;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AAAGCCCAACATGTCGGGT 21
Db 14645 AAAGCCCAACATGTCGGGT 14665
RESULT 13
AC019708 81920 bp DNA linear HTG 03-JAN-2000
LOCUS Drosophila melanogaster, *** SEQUENCING IN PROGRESS ***
DEFINITION AC019708
AC019708.1 GI:6665189
ACCESSION
VERSION
KEYWORDS HTG; HTGS PHASE2.
SOURCE Drosophila melanogaster (fruit fly)
ORGANISM Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 81920)
Adams, M. and Venter, J.C.
Direct Submission
Submitted (30-DEC-1999) Celera Genomics, 45 West Gude Drive,
Rockville, MD, USA
This sequence was identified as CPM:10210696 by the submitter.
For more information on this record e-mail to fly@celera.com.
* NOTE: This is a 'working draft' sequence.
* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.

FEATURES
SOURCE

Location/Qualifiers
1. 81920
/organism="Drosophila melanogaster"
/mol_type="genomic DNA"
/db_xref="taxon:7227"
/db_xref="taxon:7227"

BASE COUNT 24542 a 16012 c 16326 g 25040 t

ORIGIN

Query Match 84.8%; Score 17.8; DB 2; Length 81920;
Best Local Similarity 90.5%; Pred. No. 3.3e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AAAGCCCAACCATGTCGGGT 21
|||||
Db 29462 AAAGCCCAACCATGTCGGGT 29482

RESULT 14
LOCUS AC008210 153648 bp DNA linear INV 27-FEB-2001
DEFINITION Drosophila melanogaster, chromosome 3R, region 97A-97A, BAC clone
AC008210
AC008210.4 GI:13129412
HTG.

ACCESSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS

Drosophila melanogaster (fruit fly)
Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 153648)
Celnikier,S.E., Adams,M.D., Kronmiller,B., Tyler,D., Wan,K.H.,
Holt,R.A., Evans,C.A., Gocayne,J.D., Amanatides,P.G., Brandon,R.C.,
Rogers,Y., An,H., Baldwin,D., Banzon,J., Beeson,K.Y., Busam,D.A.,
Carlson,J.W., Center,A., Chame,M., Davenport,L.B., Dietz,S.M.,
Dodson,K., Dorsett,V., Doup,L.E., Doyle,C., Dresnek,D., Farfan,D.,
Fertiera,S., Frise,E., Galle,R.F., Gary,N.S., George,R.A.,
Gonzalez,M., Houch,J., Hoskins,R.A., Hostin,D., Howland,T.J.,
Ibegwan,C., Jalali,M., Kruse,D., Li,P., Mattei,B., Moshrefi,A.,
McIntosh,T.C., Moy,M., Murphy,B., Nelson,C., Nelson,K.A., Nunoo,J.,
Pacleb,J., Paragas,V., Park,S., Patel,S., Pfeiffer,B.,
Phouanavong,S., Piltman,G.S., Puri,V., Richards,S., Scheeler,F.,
Stapleton,M., Strong,R., Svitskas,R., Tector,C., Williams,S.M.,
Zaveri,J.S., Smith,H.O., Rubin,G.M. and Venter,J.C.
Sequencing of Drosophila chromosome 3R, region 97A-97A
Unpublished
2 (bases 1 to 153648)
Celnikier,S.E., Aghayani,A., Arcaina,T.T., Baxter,E., Blazej,R.G.,
Butenoff,C., Champe,M., Chavez,C., Chew,M., Ciesiolka,L.,
Doyle,C.M., Farfan,D.E., Galle,R., George,R.A., Harris,N.L.,
Hoskins,R.A., Houston,K.A., Hummasti,S.R., Karra,K., Kearney,L.,
Kim,E., Lee,B., Lewis,S., Li,P., Lomocan,M.A., Mazda,P.,
Moshrefi,A.R., Moshrefi,M., Nixon,K., Pacleb,J.M., Park,S.,
Pfeiffer,B., Poon,L., Segueira,A., Sethi,H., Sitr,E.,
Svitskas,R.R., Wan,K.H., Weinburg,T., Zhang,R., Zieran,L.L. and
Rubin,G.M.
Direct Submission
Submitted (29-JUN-1999) Drosophila Genome Center, Lawrence Berkeley
Laboratory, MS 64-121, Berkeley, CA 94720, USA
On Feb 27, 2001 this sequence version replaced gi:6633919.
Sequence submitted by:
Berkeley Drosophila Genome Project
Lawrence Berkeley National Laboratory, MS 64-121
Berkeley, CA 94720
This sequence was assembled using end sequences from a whole genome
shotgun and from subclones of this BAC and its neighboring clones.
For further information about this sequence, including its location
and relationship to other sequences, please visit our sequence
archive Web site (<http://www.fruitfly.org/sequence/>) or send email
to bdg@fruitfly.berkeley.edu.
Location/Qualifiers
1. 153648
/organism="Drosophila melanogaster"

FEATURES
SOURCE

Location/Qualifiers
1. 81920
/organism="Drosophila melanogaster"
/mol_type="genomic DNA"
/db_xref="taxon:7227"
/db_xref="taxon:7227"

BASE COUNT 45062 a 31425 c 31310 g 45851 t

ORIGIN

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Best Local Similarity 90.5%; Pred. No. 3.1e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AAAGCCCAACCATGTCGGGT 21
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Db 91650 AAAGCCCAACCATGTCGGGT 91670

RESULT 15
LOCUS AC008211/c 181905 bp DNA linear INV 24-FEB-2001
DEFINITION Drosophila melanogaster, chromosome 3R, region 97A-97A, BAC clone
AC008211/c
AC008211.9 GI:13122719
HTG.

ACCESSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS

Drosophila melanogaster (fruit fly)
Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 181905)
Celnikier,S.E., Adams,M.D., Kronmiller,B., Tyler,D., Wan,K.H.,
Holt,R.A., Evans,C.A., Gocayne,J.D., Amanatides,P.G., Brandon,R.C.,
Rogers,Y., An,H., Baldwin,D., Banzon,J., Beeson,K.Y., Busam,D.A.,
Carlson,J.W., Center,A., Champe,M., Davenport,L.B., Dietz,S.M.,
Dodson,K., Dorsett,V., Doup,L.E., Doyle,C., Dresnek,D., Farfan,D.,
Fertiera,S., Frise,E., Galle,R.F., Gary,N.S., George,R.A.,
Gonzalez,M., Houch,J., Hoskins,R.A., Hostin,D., Howland,T.J.,
Ibegwan,C., Jalali,M., Kruse,D., Li,P., Mattei,B., Moshrefi,A.,
McIntosh,T.C., Moy,M., Murphy,B., Nelson,C., Nelson,K.A., Nunoo,J.,
Pacleb,J., Paragas,V., Park,S., Patel,S., Pfeiffer,B.,
Phouanavong,S., Piltman,G.S., Puri,V., Richards,S., Scheeler,F.,
Stapleton,M., Strong,R., Svitskas,R., Tector,C., Williams,S.M.,
Zaveri,J.S., Smith,H.O., Rubin,G.M. and Venter,J.C.
Sequencing of Drosophila chromosome 3R, region 97A-97A
Unpublished
2 (bases 1 to 181905)
Celnikier,S.E., Aghayani,A., Arcaina,T.T., Baxter,E., Blazej,R.G.,
Butenoff,C., Champe,M., Chavez,C., Chew,M., Ciesiolka,L.,
Doyle,C.M., Farfan,D.E., Galle,R., George,R.A., Harris,N.L.,
Hoskins,R.A., Houston,K.A., Hummasti,S.R., Karra,K., Kearney,L.,
Kim,E., Lee,B., Lewis,S., Li,P., Lomocan,M.A., Mazda,P.,
Moshrefi,A.R., Moshrefi,M., Nixon,K., Pacleb,J.M., Park,S.,
Pfeiffer,B., Poon,L., Segueira,A., Sethi,H., Sitr,E.,
Svitskas,R.R., Wan,K.H., Weinburg,T., Zhang,R., Zieran,L.L. and
Rubin,G.M.
Direct Submission
Submitted (29-JUN-1999) Drosophila Genome Center, Lawrence Berkeley
Laboratory, MS 64-121, Berkeley, CA 94720, USA
On Feb 24, 2001 this sequence version replaced gi:7208848.
Sequence submitted by:
Berkeley Drosophila Genome Project
Lawrence Berkeley National Laboratory, MS 64-121
Berkeley, CA 94720
This sequence was assembled using end sequences from a whole genome
shotgun and from subclones of this BAC and its neighboring clones.
For further information about this sequence, including its location
and relationship to other sequences, please visit our sequence
archive Web site (<http://www.fruitfly.org/sequence/>) or send email

to bdgpe@fruitfly.berkeley.edu.
FEATURES
source

1. 181905
Location/Qualifiers
/organism="Drosophila melanogaster"
/mol_type="genomic DNA"
/strain="y; cn bw sp"
/db_xref="taxon:7227"
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/map="97A-97A"
/clone_1b="RPCI-98 (Roswell Park Cancer Institute
Drosophila melanogaster BAC library, partial ECORI in
PBACe3.6)"

BASE COUNT 55481 a 36378 c 36144 g 53902 t
ORIGIN

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Best Local Similarity 90.5%; Pred. No. 3e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 AAAGCCCAACATGTCGGGT 21
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Db 149393 AAAGCCCACTTGTGCGGT 149373

Search completed: February 12, 2004, 04:41:41
Job time : 620.146 secs

XX WPI; 2001-611728/70.
DR Genotyping an alpha-2B, 2A, or 2C adrenergic receptor gene useful for
XX determining whether an individual is at increased risk of developing a
PT disease associated with the corresponding receptor comprises detecting
PT a polymorphic site -
XX
XX Claim 10; Page 112; 163pp; English.
XX
XX The invention relates to genotyping an alpha-2B, 2A, or 2C adrenergic
CC receptor gene (I)-(III) by detecting a polymorphic site, comprising:
CC (a) obtaining a sample having a polynucleotide encoding an alpha-2B,
CC alpha2A or alpha2C or fragment or complement of; and
CC (b) detecting a polymorphic site comprising nucleotide positions 901-909
CC of (I), a site comprising cytosine or guanine at position 753 of (IIIV)
CC or a site comprising (A) (999ggcgggcg) or (B) (ggggcggtgag) at
CC positions 961-972 of (III). The method may be used for genotyping an
CC alpha2B, alpha2A or alpha2C receptor gene and further used to determine
CC whether an individual is at increased risk of developing a disease
CC associated with alpha2B, alpha2A or alpha2, comprising detecting a
CC polymorphic site which correlate to disease selected from cardiovascular
CC disease, central nervous system disease and combinations of these. In
CC addition, the technique may be used to predict an individual's response
CC to an alpha2B, alpha2A, or alpha2C agonist (e.g. ephedrine,
CC norepinephrine, clonidine, oxymetazoline, guanabenz, UK14304, BHT933 and
CC combinations of these) or antagonist (e.g. yohimbine, prazosin, ARC 239,
CC rauwolfine, idazoxan, tolazoline, phenolamine and combinations of
CC these) by detecting the polymorphic site and correlating the site to a
CC predetermined response (where the response is correlated to adenylyl
CC cyclase, MAP kinase activity, phosphorylation or inositol phosphate
CC levels). The present sequence is that of a human alpha-2BAR PCR primer,
CC useful for the genotyping methods of the invention.
XX
XX
SQ Sequence 21 BP; 5 A; 7 C; 6 G; 3 T; 0 other;
Query Match 100.0%; Score 21; DB 23; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.86;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 AAAGCCCAACCATGTCGGGT 21
Db 1 AAAGCCCAACCATGTCGGGT 21
RESULT 2
ABN32100/c
ID ABN32100 standard; DNA; 65 BP.
XX
XX
AC ABN32100;
XX
XX 15-JUL-2002 (first entry)
XX
XX Rat spliced transcript detection oligonucleotide SEQ ID NO:4848.
DE Human; mouse; rat; splice transcript; detection; RNA transcript;
XX splice variant; transcriptome; oligonucleotide library; ss.
XX
XX Rattus norvegicus.
XX
XX W0200210449-A2.
XX
XX 07-FEB-2002.
XX
XX 20-JUL-2001; 2001WO-IB01903.
XX
XX 28-JUL-2000; 2000US-221607P.
XX
XX 02-MAY-2001; 2001US-287724P.
XX
XX (COMP-) COMPUGEN INC.
XX
XX Shoshan A, Wasserman A, Mintz E, Mintz L, Faigler S;

DR WPI; 2002-257363/30.
XX
XX New oligonucleotide libraries comprising oligonucleotides which
PT selectively hybridize to mRNAs transcribed from a transcription unit of
PT a genome, useful for detecting tissue-, pathology-, and
PT developmental-specific genes -
XX
XX Example 1; SEQ ID 4848; 47pp; English.
XX
XX The present invention describes oligonucleotide libraries for detecting
CC messenger RNAs that populate a (sub-)transcriptome, where the
CC (sub-)transcriptome comprises messenger RNAs transcribed from multiple
CC transcription units that populate a genome. The library comprises
CC several oligonucleotides, each capable of hybridizing selectively to a
CC set of messenger RNAs transcribed from a given transcription unit of
CC the genome, which encodes one or more messenger RNA splice variants.
CC The oligonucleotide libraries are useful for detecting mRNAs from a
CC biological sample, in expression profiling studies, in qualitatively or
CC quantitatively characterizing the corresponding transcriptome, and in
CC detecting RNA transcripts and splice variants of human or animal
CC transcriptomes. The libraries may also be used as specialised mini
CC libraries to detect transcripts of a sub-transcriptome under a
CC particular biological or pathological state, and so allowing the
CC detection of tissue- and pathology-specific genes such as those genes
CC only expressed in specific tissue under a specific pathological
CC condition; to detect developmental specific genes; and to detect RNA
CC transcripts and splice variants of a transcriptome of a patient suffering
CC from a particular disorder. ABN27253 to ABN59589 represent
CC oligonucleotide sequences from rats, humans and mice, which are used in
CC the exemplification of the present invention.
CC N.B. The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
XX
SQ Sequence 65 BP; 13 A; 22 C; 21 G; 9 T; 0 other;
Query Match 100.0%; Score 21; DB 24; Length 65;
Best Local Similarity 100.0%; Pred. No. 0.93;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 AAAGCCCAACCATGTCGGGT 21
Db 45 AAAGCCCAACCATGTCGGGT 25
RESULT 3
AAD04761/c
ID AAD04761 standard; DNA; 1344 BP.
XX
XX
AC AAD04761;
XX
XX 04-JUL-2001 (first entry)
XX
XX Human alpha2B-adrenoceptor (alpha2B-AR) variant gene.
DE Human; cardiac; gene therapy; alpha2B-adrenoceptor; alpha2B-AR;
XX glutamic acid repeat; intracellular loop; chromosome 2; catecholamine;
XX norepinephrine; epinephrine; therapy; vascular contraction; variant;
XX coronary artery; coronary heart disease; CHD; chronic angina pectoris;
XX acute myocardial infarction; AMI; Prinzmetal's variant; db.
XX
XX Homo sapiens.
XX
XX
XX Key Location/Qualifiers
FH CDS 1..1344
FT /tag= a
FT /product= "Human alpha2B-adrenoceptor (alpha2B-AR)
XX variant protein"
XX
XX W0200129082-A1.
XX
XX 26-APR-2001.

PF 20-OCT-2000; 2000WO-FI00913.
 XX
 PR 22-OCT-1999; 99US-04222985.
 XX
 XX (JUVA-) JUVAANTIA PHARMA LTD OY.
 XX
 PI Snappi A, Heinonen P, Alhopuro P, Karvonen M, Koulu M, Pesonen U,
 PI Scheinin M, Salonen JT, Tuomala T, Lakka TA, Nyysoskenen K;
 PI Salonen R, Kaahenen J, Valkonen V;
 XX
 DR WPI; 2001-300318/31.
 DR P-PSDB; AAE00989.
 XX
 PT New DNA molecule encoding variant specific adrenoceptor protein with
 PT deletion of specific amino acids located in the third intracellular
 PT loop of the polypeptide, for treating vascular contraction of coronary
 PT arteries -
 XX
 PS Claim 3; Page 24-26; 37pp; English.
 XX
 CC The present sequence is a gene encoding human alpha2B-adrenoceptor
 CC (alpha2B-AR) variant protein. Alpha2B-AR has a glutamic acid repeat
 CC element (amino acids 298-309) of 12 glutamates, in an acidic stretch of
 CC 18 amino acids (amino acids 294-311), located in the third intracellular
 CC loop of the receptor polypeptide. The variant is obtained by deletion of
 CC three glutamates from the Glu repeat (amino acids 307-309). Alpha2B-AR
 CC gene is located on chromosome 2. Alpha2-AR mediate many of the
 CC physiological effects of the catecholamines, norepinephrine and
 CC epinephrine. An antagonist of alpha2B-adrenoceptor is useful for treating
 CC a mammal suffering from vascular contraction of coronary arteries and a
 CC disease involving vascular contraction of coronary arteries which is
 CC clinically expressed as coronary heart disease (CHD), unstable chronic
 CC angina pectoris which is clinically expressed as Prinzmetal's variant
 CC form or acute myocardial infarction (AMI). Alpha2B-AR gene is used in
 CC gene therapy.
 XX
 SQ Sequence 1344 BP; 219 A; 459 C; 400 G; 266 T; 0 other;
 XX
 Query Match 100.0%; Score 21; DB 22; Length 1344;
 Best Local Similarity 100.0%; Pred. No. 1.1;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX
 QY 1 AAAGCCCAACATGTCGGGT 21
 DB 686 AAAGCCCAACATGTCGGGT 666
 XX
 RESULT 4
 AA199906/c
 ID AA199906 standard; DNA; 1344 BP.
 XX
 AC AA199906;
 XX
 DT 18-FEB-2002 (first entry)
 XX
 DE Human alpha-2BAR third intracellular loop variant encoding DNA.
 XX
 KW Human; genotyping; alpha-2B; alpha-2A; alpha-2C; adrenergic receptor;
 KW polymorphic site; allelic variant; cardiovascular disease;
 KW central nervous system disease; adenylyl cyclase; MAP kinase activity;
 KW phosphorylation; inositol phosphate; alpha-2BAR; chromosome 2; ds.
 XX
 OS Homo sapiens.
 XX
 PH Key Location/Qualifiers
 FT 1..1344
 FT /tag= a
 FT /product= "alpha-2BAR"
 FT /note= "sequence is deleted for a 9 nucleotide
 FT polymorphic site found at nucleotides 901-909
 FT of the wildtype alpha-2BAR protein (AA199905)"
 XX
 PN WO200179561-A2.

XX
 PD 25-OCT-2001.
 XX
 XX 17-APR-2001; 2001WO-US12575.
 PF
 XX
 XX 17-APR-2000; 2000US-0551744.
 PR 10-AUG-2000; 2000US-0636259.
 PR 19-OCT-2000; 2000US-0692077.
 XX
 PA (LIGG/) LIGGETT S B.
 PA (SMAL/) SMALL K M.
 XX
 XX Liggett SB, Small KM;
 PI
 XX
 DR WPI; 2001-611728/70.
 DR P-PSDB; AAM52118.
 XX
 PT Genotyping an alpha-2B, 2A, or 2C adrenergic receptor gene useful for
 PT determining whether an individual is at increased risk of developing a
 PT disease associated with the corresponding receptor comprises detecting
 PT a polymorphic site -
 XX
 PS Claim 5; Page 144-145; 163pp; English.
 XX
 CC The invention relates to genotyping an alpha-2B, 2A, or 2C adrenergic
 CC receptor gene (I)-(III) by detecting a polymorphic site, comprising:
 CC (a) obtaining a sample having a polynucleotide encoding an alpha-2B,
 CC alpha2A or alpha2C or fragment or complement of; and
 CC (b) detecting a polymorphic site comprising nucleotide positions 901-909
 CC of (I), a site comprising cytosine or guanine at position 753 of (IIIV)
 CC or a site comprising (A) (GGGCGCGGCG) or (B) (GGGCGCGTGA) at
 CC positions 961-972 of (III). The method may be used for genotyping an
 CC alpha2B, alpha2A or alpha2C receptor gene and further used to determine
 CC whether an individual is at increased risk of developing a disease
 CC associated with alpha2B, alpha2A or alpha2C, comprising detecting a
 CC polymorphic site which correlate to disease selected from cardiovascular
 CC disease, central nervous system disease and combinations of these. In
 CC addition, the technique may be used to predict an individual's response
 CC to an alpha2B, alpha2A, or alpha2C agonist (e.g. epinephrine,
 CC norepinephrine, clonidine, oxymetazoline, guanadrel, UK14304, BHT933 and
 CC combinations of these) or antagonist (e.g. yohimbine, prazosin, ARC 239,
 CC rauwolfine, idazoxan, tolazoline, phenolamine and combinations of
 CC these) by detecting the polymorphic site and correlating the site to a
 CC predetermined response (where the response is correlated to adenylyl
 CC cyclase, MAP kinase activity, phosphorylation or inositol phosphate
 CC levels). The present sequence is that of the third intracellular loop of
 CC the human alpha-2BAR variant, the sequence is deleted for a 9 nucleotide
 CC polymorphic site found at nucleotides 901-909 of the wildtype gene
 CC (AA199905).
 XX
 SQ Sequence 1344 BP; 220 A; 458 C; 400 G; 266 T; 0 other;
 XX
 Query Match 100.0%; Score 21; DB 23; Length 1344;
 Best Local Similarity 100.0%; Pred. No. 1.1;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX
 QY 1 AAAGCCCAACATGTCGGGT 21
 DB 686 AAAGCCCAACATGTCGGGT 666
 XX
 RESULT 5
 AAD44388/c
 ID AAD44388 standard; DNA; 1344 BP.
 XX
 AC AAD44388;
 XX
 DT 13-DEC-2002 (first entry)
 XX
 DE Human alpha-2B-adrenoceptor variant DNA.
 XX
 KW Human; hypertension; alpha-2B-adrenoceptor; AR; antihypertensive;
 KW hypertension; hypotensive; variant; gene; ds.

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XX OS Homo sapiens.
OS Synthetic.
XX Key
FH CDS 1..1344
FT /tag= a
FT /product= "Human alpha-2B-adrenoceptor variant
XX protein"
XX PN
XX WO200266617-A1.
XX PD
XX 29-AUG-2002.
XX PF
XX 13-FEB-2002; 2002WO-FI00113.
XX PR
XX 20-FEB-2001; 2001FI-0000323.
XX PA
XX (JURI-) JURILAB LTD OY.
XX FI
XX Salonen J;
XX DR
XX WPI: 2002-667063/71.
XX P-PSDB; AAE26633.
XX PS
XX Disclosure; Page 24-26; 35pp; English.
XX CC
XX The invention relates to a method for detecting a risk of hypertension
XX CC by determining the pattern of alleles encoding a variant alpha-2B-
XX CC adrenoceptor (AR) protein. The methods and compositions of the invention
XX CC are useful for detecting risks and targeting treatment for hypertension.
XX CC The kit is also useful for selecting for clinical drug trials testing
XX CC the antihypertensive effect of compounds. The present sequence is human
XX CC alpha-2B-adrenoceptor variant DNA.
XX SQ
XX Sequence 1344 BP; 219 A; 459 C; 400 G; 266 T; 0 other;
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XX Query Match
XX Best Local Similarity 100.0%; Score 21; DB 24; Length 1344;
XX Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 AAAGCCCCCAGTCGCGGT 21
XX DB 686 AAAGCCCCCAGTCGCGGT 666
XX
XX RESULT 6
XX AAD04762/C
XX ID AAD04762 standard; DNA; 1353 BP.
XX AC
XX AAD04762;
XX DT
XX 04-JUL-2001 (first entry)
XX DE
XX Human alpha2B-adrenoceptor (alpha2B-AR) gene.
XX KW
XX Human; cardiac; gene therapy; alpha2B-adrenoceptor; alpha2B-AR;
XX KW glutamic acid repeat; intracellular loop; chromosome 2; catecholamine;
XX KW norepinephrine; epinephrine; therapy; vascular contraction;
XX KW coronary artery; coronary heart disease; CHD; chronic angina
XX KW acute myocardial infarction; AMI; Prinzmetal's variant; ds.
XX OS
XX Homo sapiens.
XX Key
XX CDS
XX Location/Qualifiers
XX 1..1353
XX /tag= a
XX /product= "Human alpha2B-adrenoceptor (alpha2B-AR)

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XX XX WO200123082-A1.
XX EN
XX 26-APR-2001.
XX PD
XX 20-OCT-2000; 2000WO-FI00913.
XX PF
XX 22-OCT-1999; 99US-0422985.
XX PR
XX (JUVIA-) JUVANTIA PHARMA LTD OY.
XX PA
XX Snapir A, Heimonen P, Alhopuro P, Karonen M, Koulu M, Pesonen U;
XX PI Scheinin M, Salonen JT, Tuomainen T, Lakka TA, Nyyssönen K;
XX PI Salonen R, Kauphanen J, Valkonen V;
XX DR
XX WPI: 2001-300318/31.
XX P-PSDB; AAE00990.
XX PS
XX New DNA molecule encoding variant specific adrenoceptor protein with
XX PT deletion of specific amino acids located in the third intracellular
XX PT loop of the polypeptide, for treating vascular contraction of coronary
XX PT arteries -
XX CC
XX Disclosure; Page 27-29; 37pp; English.
XX CC
XX The present sequence is a gene encoding human alpha2B-adrenoceptor
XX CC (alpha2B-AR) protein. Alpha2B-AR has a glutamic acid repeat element
XX CC (amino acids 298-309) of 12 glutamates, in an acidic stretch of 18 amino
XX CC acids (amino acids 294-311), located in the third intracellular loop of
XX CC the receptor polypeptide. Alpha2B-AR gene is located on chromosome 2.
XX CC Alpha2-AR mediate many of the physiological effects of the
XX CC catecholamines, norepinephrine and epinephrine. An antagonist of
XX CC alpha2B-adrenoceptor is useful for treating a mammal suffering from
XX CC vascular contraction of coronary arteries and a disease involving
XX CC vascular contraction of coronary arteries which is clinically expressed
XX CC as coronary heart disease (CHD), unstable chronic angina pectoris which is
XX CC clinically expressed as Prinzmetal's variant form or acute myocardial
XX CC infarction (AMI). Alpha2B-AR gene is used in gene therapy.
XX SQ
XX Sequence 1353 BP; 223 A; 459 C; 405 G; 266 T; 0 other;
XX
XX Query Match
XX Best Local Similarity 100.0%; Score 21; DB 22; Length 1353;
XX Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 AAAGCCCCCAGTCGCGGT 21
XX DB 686 AAAGCCCCCAGTCGCGGT 666
XX
XX RESULT 7
XX AA199905/C
XX ID AA199905 standard; DNA; 1353 BP.
XX AC
XX AA199905;
XX DT
XX 18-FEB-2002 (first entry)
XX DE
XX Human alpha-2BAR third intracellular loop encoding DNA.
XX KW
XX Human; genotyping; alpha-2B; alpha-2A; alpha-2C; adrenergic receptor;
XX KW polymorphic site; allelic variant; cardiovascular disease;
XX KW central nervous system disease; adenylyl cyclase; MAP kinase activity;
XX KW phosphorylation; inositol phosphate; alpha-2BAR;
XX KW GenBank Accession AF009500; chromosome 2; ds.
XX OS
XX Homo sapiens.
XX Key
XX CDS
XX Location/Qualifiers
XX 1..1353
XX /tag= a
XX /product= "alpha-2BAR"
XX /note= "sequence includes a 9 nucleotide polymorphic site

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FT at nucleotides 901-909 absent in the alpha-2BAR
 variant (AAI99906).
 XX WO200179561-A2.
 PN 25-OCT-2001.
 XX 17-APR-2001; 2001WO-US12575.
 XX 17-APR-2000; 2000US-0551744.
 PR 10-AUG-2000; 2000US-0636259.
 PR 19-OCT-2000; 2000US-0692077.
 XX (LIG6/) LIGGETT S B.
 PA (SMAL/) SMALL K M.
 XX Liggett SB, Small KM,
 PI WPI; 2001-611728/70.
 DR P-PSDB; AAMS2117.
 XX
 XX Genotyping an alpha-2B, 2A, or 2C adrenergic receptor gene useful for
 PT determining whether an individual is at increased risk of developing a
 PT disease associated with the corresponding receptor comprises detecting
 PT a polymorphic site -
 XX
 PS Claim 4; Page 144; 163pp; English.
 CC The invention relates to genotyping an alpha-2B, 2A, or 2C adrenergic
 CC receptor gene (I)-(III) by detecting a polymorphic site, comprising;
 CC (a) obtaining a sample having a polynucleotide encoding an alpha-2B,
 CC alpha2A or alpha2C or fragment or complement of; and
 CC (b) detecting a polymorphic site comprising nucleotide positions 901-909
 CC of (I), a site comprising cytosine or guanine at position 753 of (IIIV)
 CC or a site comprising (A) (ggggcgggcg) or (B) (ggggcggtcgag) at
 CC positions 961-972 of (III). The method may be used for genotyping an
 CC alpha2B, alpha2A or alpha2C receptor gene and further used to determine
 CC whether an individual is at increased risk of developing a disease
 CC associated with alpha2B, alpha2A or alpha2, comprising detecting a
 CC polymorphic site which correlate to disease selected from cardiovascular
 CC disease, central nervous system disease and combinations of these. In
 CC addition, the technique may be used to predict an individual's response
 CC to an alpha2B, alpha2A, or alpha2C agonist (e.g. epinephrine,
 CC norepinephrine, clonidine, oxymetazoline, guanabenz, UK14304, BHT933 and
 CC combinations of these) or antagonist (e.g. yohimbine, prazosin, ARC 239,
 CC rauwolfine, idazoxan, tolazoxan, phentolamine and combinations of
 CC these) by detecting the polymorphic site and correlating the site to a
 CC predetermined response (where the response is correlated to adenylyl
 CC cyclase, MAP kinase activity, phosphorylation or inositol phosphate
 CC levels). The present sequence is that of the third intracellular loop of
 CC the human alpha-2BAR (GenBank accession AF099500), the sequence includes
 CC a 9 nucleotide polymorphic site at nucleotides 901-909, absent in the
 CC alpha-2BAR variant (AAI99906).
 CC
 XX
 SQ Sequence 1353 BP; 224 A; 458 C; 405 G; 266 T; 0 other;
 Query Match 100.0%; Score 21; DB 23; Length 1353;
 Best Local Similarity 100.0%; Pred. No. 1.1;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DE Human alpha-2B-adrenoceptor gene.
 XX
 KM Human; hypertension; alpha-2B-adrenoceptor; AR; antihypertensive;
 KM hypertension; hypotensive; gene; ds.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT CDS 1..1353
 FT /*tag= a
 FT /product= "Human alpha-2B-adrenoceptor protein"
 PN WO200266617-A1.
 XX
 PD 29-AUG-2002.
 XX
 PF 13-FEB-2002; 2002WO-FI00113.
 XX
 PR 20-FEB-2001; 2001FI-0000323.
 XX
 PA (JURI-) JURILAB LTD OY.
 PI Salonen J;
 XX
 XX WPI; 2002-667063/71.
 DR P-PSDB; AAE26634.
 XX
 PT Detecting a risk of hypertension and targeting treatment in a subject
 PT by determining the pattern of alleles encoding a variant
 PT alpha-2-adrenoceptor -
 XX
 PS Disclosure; Page 27-29; 35pp; English.
 CC The invention relates to a method for detecting a risk of hypertension
 CC by determining the pattern of alleles encoding a variant alpha-2B-
 CC adrenoceptor (AR) protein. The methods and compositions for the invention
 CC are useful for detecting risks and targeting treatment for hypertension.
 CC The kit is also useful for selecting for clinical drug trials testing
 CC the antihypertensive effect of compounds. The present sequence is human
 CC alpha-2B-adrenoceptor gene.
 CC
 XX
 SQ Sequence 1353 BP; 223 A; 459 C; 405 G; 266 T; 0 other;
 Query Match 100.0%; Score 21; DB 24; Length 1353;
 Best Local Similarity 100.0%; Pred. No. 1.1;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAAGCCCAACATGTCGGGT 21
 |||||
 DB 686 AAAGCCCAACATGTCGGGT 666

RESULT 9
 AAQ14151/c
 ID AAQ14151 standard; DNA; 2064 BP.
 XX
 AC AAQ14151;
 XX
 DT 06-JAN-1992 (first entry)
 XX
 DE Human alpha 2 beta adrenergic receptor gene.
 XX
 KM Neurotransmission; adrenaline; epinephrine; NGC-alpha2beta; ss.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT CDS 288..1752
 FT /*tag= a
 XX
 XX US5053337-A.
 PN
 XX 01-OCT-1991.

```

XX 30-OCT-1989; 89US-0428856.
XX 30-OCT-1989; 89US-0428856.
XX (NEUR-) NEUROGENETIC CORP.
XX Weinsbank RL, Hartig PR;
XX WPI; 1991-310087/42.
XX P-PsDB; AARI4149.
XX Isolated DNA encoding human adrenergic receptor - for detecting
XX nucleic acids encoding alpha, 2-beta adrenergic receptor, for
XX screening drugs.
XX Claim 1; Fig 2; 15pp; English.
XX CC Clone NGC-alpha2beta was isolated from a human spleen genomic
XX library by screening with a fragment of the human 5-HT1A receptor
XX gene. The gene can be used to express recombinant receptor protein
XX which can be used to produce antibodies for inhibition of receptor
XX function.
XX SQ Sequence 2064 BP; 319 A; 696 C; 659 G; 390 T; 0 other;
Query Match 100.0%; Score 21; DB 12; Length 2064;
Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AAGCCCCCAGCATGTCGGGT 21
Db 1084 AAGCCCCCAGCATGTCGGGT 1064
RESULT 10
ID AAT59499 standard; DNA; 2064 BP.
AC AAT59499;
XX 25-MAR-2003 (updated)
DT 06-MAY-1997 (first entry)
XX Human alpha-2b adrenergic receptor genomic DNA clone.
DE Human alpha-2b adrenergic receptor genomic DNA clone.
XX Alpha-2b adrenergic receptor; adrenoceptor; adrenaline;
XX epinephrine; signal transduction; neurotransmitter; ligand; ss.
XX Homo sapiens.
OS Homo sapiens.
XX Key Location/Qualifiers
XX CDS 288..1751
XX /tag= a
XX USS595880-A.
XX 21-JAN-1997.
XX 22-OCT-1992; 92US-0965040.
XX 30-OCT-1989; 89US-0428856.
XX 30-MAY-1991; 91US-0707604.
XX 22-OCT-1992; 92US-0965040.
XX (SYNA-) SYNAPTIC PHARM CORP.
XX PI Hartig PR, Weinsbank RL;
XX WPI; 1997-107576/10.
XX P-PsDB; AAW11804.
XX Assay for alpha-2b adrenergic receptor ligands - using membranes of

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PT cells expressing recombinant receptor
XX Disclosure; Fig 2A-E; 16pp; English.
XX A genomic DNA clone (AAT59499) codes for human alpha-2b adrenergic
XX receptor (AAW11804), a member of the rhodopsin-like signal transducer
XX family. It was isolated from a human spleen genomic library in the
XX lambda vector Charon 28 by screening with a 1.6 kb fragment of the
XX human 5-hydroxytryptamine receptor gene. Plasmid pNGC-alpha-2b
XX comprising DNA encoding the alpha-2b adrenoceptor is deposited as
XX ATCC 68144. Vectors have been adapted to allow prodn. of alpha-2b
XX adrenoceptor in bacterial, yeast or mammalian cells; transfected
XX Ltk- cells, designated L-NGC-alpha-2b, are deposited as ATCC CRL
XX 10275. Membranes of such cells can be used in novel methods to
XX identify drugs which specifically interact with, and bind to, the
XX alpha-2b adrenergic receptor.
XX (Updated on 25-MAR-2003 to correct PF field.)
XX SQ Sequence 2064 BP; 319 A; 696 C; 659 G; 390 T; 0 other;
Query Match 100.0%; Score 21; DB 18; Length 2064;
Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AAGCCCCCAGCATGTCGGGT 21
Db 1084 AAGCCCCCAGCATGTCGGGT 1064
RESULT 11
ID ACA56583/c
ID ACA56583 standard; cDNA; 2072 BP.
AC ACA56583;
XX 06-JUN-2003 (first entry)
XX Human signalling pathway polynucleotide probe SEQ ID NO 1181.
DE Human signalling pathway polynucleotide probe SEQ ID NO 1181.
XX Human; probe; ss; array element; Parkinson's disease;
XX signalling pathway population; cancer; adenocarcinoma; leukaemia;
XX immunopathy; AIDS; asthma; neuropathy; Alzheimer's disease; microarray.
XX Homo sapiens.
OS Homo sapiens.
XX USS650938-B1.
XX 31-DEC-2002.
XX 30-JAN-1998; 98US-0016434.
XX 30-JAN-1998; 98US-0016434.
XX (INCY-) INCYTE GENOMICS INC.
XX Au-Young J, Sellhammer JJ;
XX WPI; 2003-352189/33.
XX Combination of polynucleotide probes, useful as array elements in a
XX microarray for monitoring the expression of a number of target
XX polynucleotides -
XX Claim 1; SEQ ID NO 1181, 65pp; English.
XX The invention relates to a combination which, comprises a number of
XX polynucleotide probes comprising a sequence selected from one of the 1490
XX sequences mentioned in the specification. The combination is useful as an
XX array element in a microarray for monitoring the expression of a number
XX of target polynucleotides. The microarray is particularly useful in the
XX diagnosis and treatment of cancer and immunopathology and neuropathology.
XX The microarray is useful in diagnostics and treatment regimens, drug
XX discovery and development, toxicological and carcinogenicity studies,

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XX The invention relates to isolated polynucleotide (I) and
CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
CC and gene mapping, and in recombinant production of (II). The
CC polynucleotides are also used in diagnostics as expressed sequence tags
CC for identifying expressed genes. (I) is useful in gene therapy techniques
CC to restore normal activity of (II) or to treat disease states involving
CC (II). (II) is useful for generating antibodies against it, detecting or
CC quantitating a polypeptide in tissue, as molecular weight markers and as
CC a food supplement. (II) and its binding partners are useful in medical
CC imaging of sites expressing (II). (I) and (II) are useful for treating
CC disorders involving aberrant protein expression or biological activity.
CC The polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensic, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. AA564197-AAS94564 represent novel human
CC diagnostic coding sequences of the invention.
CC Note: The sequence data for this patent did not appear in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.

XX
SQ Sequence 1755 BP; 349 A; 589 C; 545 G; 271 T; 1 other;

QY Query Match 82.9%; Score 17.4; DB 23; Length 1755;
Best Local Similarity 94.7%; Pred. No. 67;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

DB 630 AAAGCCCCCAGTGTGCG 612

QY 1 AAAGCCCCCAGTGTGCG 19
|||||
|||||

DB 1755 AAAGCCCCCAGTGTGCG 1755
|||||
|||||

RESULT 14
ABV07991 ID ABV07991 standard; CDNA; 447 BP.

XX
AC ABV07991;
XX
DT 13-SEP-2002 (first entry)
XX
DE Human prostate expression marker CDNA 7982.
XX
KW Human; prostate cancer; cytosolic; carcinogen; pharmacodynamic marker;
KW pharmacogenomic marker; gene; ss.
XX
OS Homo sapiens.
XX
PN WO200160860-A2.
XX
PD 23-AUG-2001.
XX
PF 20-FEB-2001; 2001WO-US05171.
XX
PR 17-FEB-2000; 2000US-18313P.
XX
PR 16-MAR-2000; 2000US-189862P.
XX
PR 25-MAY-2000; 2000US-207454P.
XX
PR 09-JUN-2000; 2000US-211314P.
XX
PR 18-JUL-2000; 2000US-219007P.
XX
PR 13-DEC-2000; 2000US-255281P.
XX
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX
PI Schlegel R, Endege WO, Monahan JE;
XX
DR WPI; 2001-662795/76.
XX
PT Novel isolated nucleic acid molecule associated with cancerous state of
PT prostate cells and correlating with presence of prostate cancer, useful
PT for detecting presence of prostate cancer, stage of prostate cancer -
XX
PS Claim 1; Page 1278; 11750pp; English.

XX The invention relates to an isolated nucleic acid molecule (I) comprising
CC a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the
CC specification or its complement. (I) is useful for:
CC (a) assessing whether a patient is afflicted with prostate cancer;
CC (b) monitoring the progression of prostate cancer in a patient;
CC (c) assessing the efficacy of a test compound to inhibit prostate
CC cancer in a patient;
CC (d) assessing the efficacy of a therapy for inhibiting prostate cancer
CC in a patient;
CC (e) selecting a composition for inhibiting prostate cancer in a patient;
CC (f) assessing the prostate cell carcinogenic potential of a compound;
CC (g) determining whether prostate cancer has metastasized in a patient;
CC (h) assessing the aggressiveness or indolence of prostate cancer in a
CC patient;
CC (I) is also useful as a pharmacodynamic or pharmacogenomic marker.

XX
SQ Sequence 447 BP; 144 A; 99 C; 90 G; 114 T; 0 other;

QY Query Match 80.0%; Score 16.8; DB 23; Length 447;
Best Local Similarity 90.0%; Pred. No. 1.2e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

DB 378 AAAGCCCCCAGTGTGCG 397

QY 1 AAAGCCCCCAGTGTGCG 20
|||||
|||||

DB 447 AAAGCCCCCAGTGTGCG 447
|||||
|||||

RESULT 15
ABA12198 ID ABA12198 standard; CDNA; 990 BP.

XX
AC ABA12198;
XX
DT 23-JAN-2002 (first entry)
XX
DE Human nervous system related polynucleotide SEQ ID NO 1205.
XX
KW Human; nocotropic; neuroprotective; cytosolic; dermatological; virucide;
KW immunosuppressive; anti-inflammatory; anti-HIV; antibacterial; vulnery;
KW antiparkinsonian; antiskinning; antianaemic; antiarthritic; cancer;
KW antineumatic; hepatotropic; cerebroprotective; antiinflammatory;
KW antiallergic; antidiabetic; antitumor; anticonvulsant; antifungal;
KW antiparasitic; cardiac; immune disorder; cardiovascular disorder;
KW neurological disease; infection; nephrotropic; gene therapy; vaccine; ss.
XX
OS Homo sapiens.
XX
PN WO200159063-A2.
XX
PD 16-AUG-2001.
XX
PF 17-JAN-2001; 2001WO-US01334.
XX
PR 31-JAN-2000; 2000US-0179065.
XX
PR 04-FEB-2000; 2000US-0180628.
XX
PR 24-FEB-2000; 2000US-0184664.
XX
PR 02-MAR-2000; 2000US-0186350.
XX
PR 16-MAR-2000; 2000US-0189874.
XX
PR 17-MAR-2000; 2000US-0190076.
XX
PR 18-APR-2000; 2000US-0198123.
XX
PR 19-MAY-2000; 2000US-0205515.
XX
PR 07-JUN-2000; 2000US-0209467.
XX
PR 28-JUN-2000; 2000US-0214886.
XX
PR 30-JUN-2000; 2000US-0215135.
XX
PR 07-JUL-2000; 2000US-0216647.
XX
PR 07-JUL-2000; 2000US-0216880.
XX
PR 11-JUL-2000; 2000US-0217487.
XX
PR 11-JUL-2000; 2000US-0217496.
XX
PR 14-JUL-2000; 2000US-0218290.
XX
PR 26-JUL-2000; 2000US-0220963.
XX
PR 26-JUL-2000; 2000US-0220964.
XX
PR 14-AUG-2000; 2000US-0224518.

PR	14-AUG-2000	2000US-0224519
PR	14-AUG-2000	2000US-0225213
PR	14-AUG-2000	2000US-0225214
PR	14-AUG-2000	2000US-0225267
PR	14-AUG-2000	2000US-0225566
PR	14-AUG-2000	2000US-0225568
PR	14-AUG-2000	2000US-0225570
PR	14-AUG-2000	2000US-0225457
PR	14-AUG-2000	2000US-0225547
PR	14-AUG-2000	2000US-0225758
PR	14-AUG-2000	2000US-0225759
PR	18-AUG-2000	2000US-0226779
PR	22-AUG-2000	2000US-0226681
PR	22-AUG-2000	2000US-0226688
PR	22-AUG-2000	2000US-0227182
PR	23-AUG-2000	2000US-0227709
PR	30-AUG-2000	2000US-0228924
PR	01-SEP-2000	2000US-0229287
PR	01-SEP-2000	2000US-0229143
PR	01-SEP-2000	2000US-0229344
PR	05-SEP-2000	2000US-0229545
PR	05-SEP-2000	2000US-0229549
PR	06-SEP-2000	2000US-0229613
PR	06-SEP-2000	2000US-0230438
PR	08-SEP-2000	2000US-0231442
PR	08-SEP-2000	2000US-0231443
PR	08-SEP-2000	2000US-0231444
PR	08-SEP-2000	2000US-0231444
PR	08-SEP-2000	2000US-0231444
PR	08-SEP-2000	2000US-0231414
PR	08-SEP-2000	2000US-0232081
PR	12-SEP-2000	2000US-0231668
PR	14-SEP-2000	2000US-0232397
PR	14-SEP-2000	2000US-0232398
PR	14-SEP-2000	2000US-0232399
PR	14-SEP-2000	2000US-0232400
PR	14-SEP-2000	2000US-0232401
PR	14-SEP-2000	2000US-0233063
PR	14-SEP-2000	2000US-0233065
PR	14-SEP-2000	2000US-0233164
PR	21-SEP-2000	2000US-0234423
PR	21-SEP-2000	2000US-0234474
PR	25-SEP-2000	2000US-0234977
PR	25-SEP-2000	2000US-0235484
PR	26-SEP-2000	2000US-0235484
PR	27-SEP-2000	2000US-0235634
PR	27-SEP-2000	2000US-0235634
PR	29-SEP-2000	2000US-0236127
PR	29-SEP-2000	2000US-0236167
PR	29-SEP-2000	2000US-0236168
PR	29-SEP-2000	2000US-0236169
PR	29-SEP-2000	2000US-0236170
PR	02-OCT-2000	2000US-0236602
PR	02-OCT-2000	2000US-0237037
PR	02-OCT-2000	2000US-0237038
PR	02-OCT-2000	2000US-0237039
PR	02-OCT-2000	2000US-0237040
PR	13-OCT-2000	2000US-0239933
PR	13-OCT-2000	2000US-0239937
PR	20-OCT-2000	2000US-0240360
PR	20-OCT-2000	2000US-0241785
PR	20-OCT-2000	2000US-0241785
PR	20-OCT-2000	2000US-0241787
PR	20-OCT-2000	2000US-0241807
PR	20-OCT-2000	2000US-0241809
PR	20-OCT-2000	2000US-0242221
PR	01-NOV-2000	2000US-0244614
PR	08-NOV-2000	2000US-0244614
PR	08-NOV-2000	2000US-0244675
PR	08-NOV-2000	2000US-0246477
PR	08-NOV-2000	2000US-0246477

CC	08-NOV-2000;	2000US-0246478.
PR	08-NOV-2000;	2000US-0246523.
PR	08-NOV-2000;	2000US-0246524.
PR	08-NOV-2000;	2000US-0246525.
PR	08-NOV-2000;	2000US-0246526.
PR	08-NOV-2000;	2000US-0246527.
PR	08-NOV-2000;	2000US-0246528.
PR	08-NOV-2000;	2000US-0246532.
PR	08-NOV-2000;	2000US-0246603.
PR	08-NOV-2000;	2000US-0246610.
PR	08-NOV-2000;	2000US-0246613.
PR	17-NOV-2000;	2000US-0249207.
PR	17-NOV-2000;	2000US-0249208.
PR	17-NOV-2000;	2000US-0249209.
PR	17-NOV-2000;	2000US-0249210.
PR	17-NOV-2000;	2000US-0249211.
PR	17-NOV-2000;	2000US-0249212.
PR	17-NOV-2000;	2000US-0249213.
PR	17-NOV-2000;	2000US-0249214.
PR	17-NOV-2000;	2000US-0249215.
PR	17-NOV-2000;	2000US-0249216.
PR	17-NOV-2000;	2000US-0249217.
PR	17-NOV-2000;	2000US-0249218.
PR	17-NOV-2000;	2000US-0249244.
PR	17-NOV-2000;	2000US-0249245.
PR	17-NOV-2000;	2000US-0249264.
PR	17-NOV-2000;	2000US-0249265.
PR	17-NOV-2000;	2000US-0249297.
PR	17-NOV-2000;	2000US-0249299.
PR	17-NOV-2000;	2000US-0249300.
PR	01-DEC-2000;	2000US-0250391.
PR	01-DEC-2000;	2000US-0251160.
PR	05-DEC-2000;	2000US-0251030.
PR	05-DEC-2000;	2000US-0251988.
PR	05-DEC-2000;	2000US-0256719.
PR	06-DEC-2000;	2000US-0251479.
PR	08-DEC-2000;	2000US-0251856.
PR	08-DEC-2000;	2000US-0251868.
PR	08-DEC-2000;	2000US-0251869.
PR	08-DEC-2000;	2000US-0251889.
PR	08-DEC-2000;	2000US-0251990.
PR	11-DEC-2000;	2000US-0254097.
PR	05-JAN-2001;	2001US-0256978.
XX		
PA	(HUMA-) HUMAN GENOME SCI INC.	
PI	Rosen CA, Barash SC, Ruben SM;	
XX	WPI; 2001-541565/60.	
DR	P-PSDB; ABB15872.	
PT	Nucleic acids encoding 3224 human nervous system antigen polypeptides,	
PT	useful for preventing, diagnosing and/or treating nervous system	
XX	cancers and metastases -	
PS	Claim 1; SEQ ID NO 1205; 1701bp + Sequence Listing; English.	
CC	The invention relates to novel genes (ABA11004-ABA21534) and proteins	
CC	(ABBI1678-ABBI18001) useful for preventing, treating or ameliorating	
CC	medical conditions e.g. by protein or gene therapy. The genes are	
CC	isolated from a range of human tissues disclosed in the specification.	
CC	The nucleic acids, proteins, antibodies and (ant)agonists are useful	
CC	in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast	
CC	and ovarian cancer and other cancers of the adrenal gland, bone, bone	
CC	marrow, breast, gastrointestinal tract, liver, lung, or urogenital;	
CC	(b) immune disorders e.g. Addison's disease, allergies, autoimmune	
CC	hemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's	
CC	disease, multiple sclerosis, rheumatoid arthritis and ulcerative	
CC	colitis; (c) cardiovascular disorders such as myocardial ischaemias;	
CC	(d) wound healing; (e) neurological diseases e.g. cerebral anoxia and	
CC	epilepsy; and (f) infectious diseases such as viral, bacterial, fungal	
CC	and parasitic infections.	

CC Note: The sequence data for this patent did not form part of the
CC printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pat_sequences.

XX
SQ Sequence 990 BP; 193 A; 336 C; 270 G; 188 T; 3 other;

Query Match 78.1%; Score 16.4; DB 22; Length 990;
Best Local Similarity 94.4%; Pred. No. 2e+02; 1; Indels 0; Gaps 0;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 AGCCCCACCATGCTCGGG 20
|||
Db 563 AGCCCCACCATGCTCGGG 580

Search completed: February 12, 2004, 04:01:27
Job time : 114.378 secs

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAAGCCACCATGTCGGGT 21
 |||||
 Db 1098 AAAGCCACCATGTCGGGT 1078

RESULT 2
 US-09-773-426A-13/C
 ; Sequence 13, Application US/09773426A
 ; Patent No. 6534302
 ; GENERAL INFORMATION:
 ; APPLICANT: Cluckeman, Maria Alexandra
 ; APPLICANT: Williamsen, Mark
 ; APPLICANT: Teta, Fong-Ying
 ; APPLICANT: Rudolph-Owen, Laura A.
 ; TITLE OF INVENTION: 22438, 23553, 25278, and 26212 No. 6534302e1
 ; TITLE OF INVENTION: Human Sulfatases (A CIP Application)
 ; FILE REFERENCE: 35800/208398(5800-79
 ; CURRENT APPLICATION NUMBER: US/09/773, 426A
 ; PRIOR FILING DATE: 2001-01-31
 ; PRIOR APPLICATION NUMBER: US 09/495, 823
 ; NUMBER OF SEQ ID NOS: 14
 ; SOFTWARE: FASTSEQ for Windows Version 4.0
 ; SEQ ID NO 13
 ; LENGTH: 1710
 ; TYPE: DNA
 ; ORGANISM: homo sapiens
 ; US-09-773-426A-13

Query Match 75.2%; Score 15.8; DB 4; Length 1710;
 Best Local Similarity 89.5%; Pred. No. 66;
 Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 AGCCCCACCATGTCGGGT 21
 |||||
 Db 1070 AGACCACCATGTCGGGT 1052

RESULT 3
 US-08-196-989B-1
 ; Sequence 1, Application US/08196989B
 ; Patent No. 5585476
 ; GENERAL INFORMATION:
 ; APPLICANT: MacLennan, A. John
 ; TITLE OF INVENTION: Molecular Cloning and Expression of
 ; TITLE OF INVENTION: G-Protein Coupled Receptors
 ; NUMBER OF SEQUENCES: 14
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Saliwanchik & Saliwanchik
 ; STREET: 2421 N.W. 41st Street, Suite A-1
 ; CITY: Gainesville
 ; STATE: FL
 ; COUNTRY: US
 ; ZIP: 32606
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/196, 989B
 ; FILING DATE: 15-FEB-1994
 ; CLASSIFICATION: 536
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Lloyd, Jeff
 ; REGISTRATION NUMBER: 35,589
 ; REFERENCE/DOCKET NUMBER: MAC-100
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 904-375-8100
 ; TELEFAX: 904-372-5800
 ; INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:
 ;
 ; LENGTH: 2754 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: DNA (genomic)
 ; US-08-196-989B-1

Query Match 75.2%; Score 15.8; DB 1; Length 2754;
 Best Local Similarity 89.5%; Pred. No. 70;
 Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 AGCCCCACCATGTCGGGT 21
 |||||
 Db 139 AGCCCCACCATGTCGGGT 157

RESULT 4
 US-08-760-936-1
 ; Sequence 1, Application US/08760936
 ; Patent No. 5856443
 ; GENERAL INFORMATION:
 ; APPLICANT: MacLennan, A. John
 ; TITLE OF INVENTION: Molecular Cloning and Expression of
 ; TITLE OF INVENTION: G-Protein Coupled Receptors
 ; NUMBER OF SEQUENCES: 14
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Saliwanchik, Lloyd & Saliwanchik
 ; STREET: 2421 N.W. 41st Street, Suite A-1
 ; CITY: Gainesville
 ; STATE: FL
 ; COUNTRY: US
 ; ZIP: 32606
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/760, 936
 ; FILING DATE: December 6, 1996
 ; CLASSIFICATION: 536
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Pace, Doran R.
 ; REGISTRATION NUMBER: 38,261
 ; REFERENCE/DOCKET NUMBER: MAC-100C1
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 352-375-8100
 ; TELEFAX: 352-372-5800
 ; INFORMATION FOR SEQ ID NO: 1:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 2754 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: DNA (genomic)
 ; US-08-760-936-1

Query Match 75.2%; Score 15.8; DB 2; Length 2754;
 Best Local Similarity 89.5%; Pred. No. 70;
 Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 AGCCCCACCATGTCGGGT 21
 |||||
 Db 139 AGCCCCACCATGTCGGGT 157

RESULT 5
 US-09-225-024-1
 ; Sequence 1, Application US/09225024
 ; Patent No. 6518414
 ; GENERAL INFORMATION:
 ; APPLICANT: MacLennan, A. John

```

; TITLE OF INVENTION: Molecular Cloning and Expression of
; TITLE OF INVENTION: G-Protein Coupled Receptors
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Salivanchik, Lloyd & Salivanchik
; STREET: 2421 N.W. 41st Street, Suite A-1
; CITY: Gainesville
; STATE: FL
; COUNTRY: US
; ZIP: 32606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/225,024
; FILING DATE: 04-JAN-1999
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/760,936
; FILING DATE: 6-DEC-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/196,989
; FILING DATE: 15-FEB-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Pace, Doran R.
; REGISTRATION NUMBER: 38,261
; REFERENCE/DOCKET NUMBER: MAC-100C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 352-375-8100
; TELEFAX: 352-372-5800
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2754 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-09-225-024-1

Query Match      75.2%; Score 15.8; DB 4; Length 2754;
Best Local Similarity 89.5%; Pred. No. 70;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      3 AGCCCCCAGCATGTCGGGT 21
Db      139 AGCCCCCAGCATGTCGGGT 157

RESULT 6
US-09-773-426A-6/c
; Sequence 6, Application US/09773426A
; Patent No. 6534302
; GENERAL INFORMATION:
; APPLICANT: Gluckman, Maria Alexandra
; APPLICANT: Williamson, Mark
; APPLICANT: Tsai, Feng-Ying
; APPLICANT: Rudolph-Owen, Laura A.
; TITLE OF INVENTION: 22438, 23553, 25278, and 26212 No. 6534302e1
; TITLE OF INVENTION: Human Sulfatases (A CIP Application)
; FILE REFERENCE: 35800/208398(5800-79
; CURRENT APPLICATION NUMBER: US/09/773,426A
; CURRENT FILING DATE: 2001-01-31
; PRIOR APPLICATION NUMBER: US 09/495,823
; PRIOR FILING DATE: 2000-01-31
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 2940
; TYPE: DNA
; ORGANISM: homo sapiens
; FEATURE:
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; NAME/KEY: CDS
; LOCATION: (334) ... (2043)
; US-09-773-426A-6

Query Match      75.2%; Score 15.8; DB 4; Length 2940;
Best Local Similarity 89.5%; Pred. No. 70;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      3 AGCCCCCAGCATGTCGGGT 21
Db      1403 AGCCCCCAGCATGTCGGGT 1385

RESULT 7
US-09-662-250A-10
; Sequence 10, Application US/09662250A
; Patent No. 6368856
; GENERAL INFORMATION:
; APPLICANT: Bretz P. Monica
; APPLICANT: Jacqueline Wyatt
; TITLE OF INVENTION: ANTISENSE MODULATION OF PHOSPHORYLASE KINASE BETA EXPRESSION
; FILE REFERENCE: RTS-0129
; CURRENT APPLICATION NUMBER: US/09/662,250A
; CURRENT FILING DATE: 2000-09-14
; NUMBER OF SEQ ID NOS: 102
; SEQ ID NO 10
; LENGTH: 277
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (23) ... (154)
; US-09-662-250A-10

Query Match      73.3%; Score 15.4; DB 4; Length 277;
Best Local Similarity 94.1%; Pred. No. 87;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 AAAGCCCCCAGCATGTC 17
Db      157 AAAGCCCCCAGCATGTC 173

RESULT 8
US-08-469-260A-28
; Sequence 28, Application US/08469260A
; Patent No. 6451578
; GENERAL INFORMATION:
; APPLICANT: JOHN N. SIMONS
; APPLICANT: TAMI J. PILOT-MATIAS
; APPLICANT: GEORGE J. DAMSON
; APPLICANT: GEORGE G. SCHLAUDER
; APPLICANT: SURESH M. DESAI
; APPLICANT: THOMAS P. LEARY
; APPLICANT: ANTHONY SCOTT MUEBHOFF
; APPLICANT: JAMES C. ERKER
; APPLICANT: SHERI L. BUTIK
; APPLICANT: ISA K. MUSHAWAR
; TITLE OF INVENTION: NON-A, NON-B, NON-C, NON-D, NON-E HEPATITIS
; TITLE OF INVENTION: REAGENTS AND METHODS FOR THEIR USE
; NUMBER OF SEQUENCES: 716
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ABBOTT LABORATORIES D377/AP6D
; STREET: 100 ABBOTT PARK ROAD
; CITY: ABBOTT PARK
; STATE: IL
; COUNTRY: USA
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/469,260A
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/424,550
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: POREMSKI, PRISCILLA E.
REGISTRATION NUMBER: 33,207
REFERENCE/DOCKET NUMBER: 5527.PC.01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 708-937-6365
TELEFAX: 708-938-2623
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 369 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-469-260A-28

Query Match 72.4% Score 15.2; DB 4; Length 369;
Best Local Similarity 85.0%; Pred. No. 1.1e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 AAAGCCCAACATGTCGGG 20
DB 119 AAAGCCCAACATGTCGGG 138

RESULT 9
US-08-468-446-28
Sequence 28, Application US/08488446
Patent No. 6558898
GENERAL INFORMATION:
APPLICANT: JOHN N. SIMONS
APPLICANT: TAMT J. PILOT-MATTIAS
APPLICANT: GEORGE J. DAWSON
APPLICANT: GEORGE G. SCHLAUDER
APPLICANT: SURESH M. DESAI
APPLICANT: THOMAS P. LEARY
APPLICANT: ANTHONY SCOTT MUEHROFF
APPLICANT: JAMES C. ERKER
APPLICANT: SHERI L. BUIJK
APPLICANT: ISA K. MUSHAWAR
TITLE OF INVENTION: NON-A, NON-B, NON-C, NON-D, NON-E HEPATITIS
TITLE OF INVENTION: REAGENTS AND METHODS FOR THEIR USE
NUMBER OF SEQUENCES: 716
CORRESPONDENCE ADDRESS:
ADDRESSEE: ABBOTT LABORATORIES D377/APED
STREET: 100 ABBOTT PARK ROAD
CITY: ABBOTT PARK
STATE: IL
COUNTRY: USA
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/488,446
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/424,550
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: POREMSKI, PRISCILLA E.
REGISTRATION NUMBER: 33,207
REFERENCE/DOCKET NUMBER: 5527.PC.01

TELECOMMUNICATION INFORMATION:
TELEPHONE: 708-937-6365
TELEFAX: 708-938-2623
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 369 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-468-446-28

Query Match 72.4% Score 15.2; DB 4; Length 369;
Best Local Similarity 85.0%; Pred. No. 1.1e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 AAAGCCCAACATGTCGGG 20
DB 119 AAAGCCCAACATGTCGGG 138

RESULT 10
US-08-467-344A-28
Sequence 28, Application US/08467344A
Patent No. 6586568
GENERAL INFORMATION:
APPLICANT: JOHN N. SIMONS
APPLICANT: TAMT J. PILOT-MATTIAS
APPLICANT: GEORGE J. DAWSON
APPLICANT: GEORGE G. SCHLAUDER
APPLICANT: SURESH M. DESAI
APPLICANT: THOMAS P. LEARY
APPLICANT: ANTHONY SCOTT MUEHROFF
APPLICANT: JAMES C. ERKER
APPLICANT: SHERI L. BUIJK
APPLICANT: ISA K. MUSHAWAR
TITLE OF INVENTION: NON-A, NON-B, NON-C, NON-D, NON-E HEPATITIS
TITLE OF INVENTION: REAGENTS AND METHODS FOR THEIR USE
NUMBER OF SEQUENCES: 716
CORRESPONDENCE ADDRESS:
ADDRESSEE: ABBOTT LABORATORIES D377/APED
STREET: 100 ABBOTT PARK ROAD
CITY: ABBOTT PARK
STATE: IL
COUNTRY: USA
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/467,344A
FILING DATE: 07-Jun-1995
CLASSIFICATION: <unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/424,550
FILING DATE: <unknown>
ATTORNEY/AGENT INFORMATION:
NAME: POREMSKI, PRISCILLA E.
REGISTRATION NUMBER: 33,207
REFERENCE/DOCKET NUMBER: 5527.PC.01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 708-937-6365
TELEFAX: 708-938-2623
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 369 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
SEQUENCE DESCRIPTION: SEQ ID NO: 28;

US-08-467-344A-28

Query Match 72.4%; Score 15.2; DB 4; Length 369;
Best Local Similarity 85.0%; Pred. No. 1.1e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 AAAGCCACCATGTCGGG 20
DB 119 AAAGCCACCATAGCCGG 138

RESULT 11

US-09-149-476-36/c
Sequence 36, Application US/09149476
Patent No. 6420526
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: 186 Human Secreted proteins
FILE REFERENCE: P2002P1
CURRENT APPLICATION NUMBER: US/09/149,476
EARLIER APPLICATION NUMBER: PCT/US98/04493
EARLIER FILING DATE: 1998-03-06
EARLIER APPLICATION NUMBER: 60/040,162
EARLIER FILING DATE: 1997-03-07
EARLIER APPLICATION NUMBER: 60/040,333
EARLIER FILING DATE: 1997-03-07
EARLIER APPLICATION NUMBER: 60/038,621
EARLIER FILING DATE: 1997-03-07
EARLIER APPLICATION NUMBER: 60/040,626
EARLIER FILING DATE: 1997-03-07
EARLIER APPLICATION NUMBER: 60/040,334
EARLIER FILING DATE: 1997-03-07
EARLIER APPLICATION NUMBER: 60/040,336
EARLIER FILING DATE: 1997-03-07
EARLIER APPLICATION NUMBER: 60/040,163
EARLIER FILING DATE: 1997-03-07
EARLIER APPLICATION NUMBER: 60/047,600
EARLIER FILING DATE: 1997-05-23
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EARLIER APPLICATION NUMBER: 60/047,597
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EARLIER FILING DATE: 1997-05-23

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EARLIER FILING DATE: 1997-05-23
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EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,632
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,601
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/043,580
EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/043,568
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EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/048,974
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/056,886
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,877
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,889
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EARLIER APPLICATION NUMBER: 60/056,872
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EARLIER FILING DATE: 1997-08-22
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EARLIER FILING DATE: 1997-08-22
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EARLIER APPLICATION NUMBER: 60/056,910
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,864

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EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,845
EARLIER FILING DATE: 1997-08-22
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EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/057,761
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/047,595
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,599
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EARLIER APPLICATION NUMBER: 60/047,588
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,585
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EARLIER FILING DATE: 1997-05-23
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EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,593
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EARLIER APPLICATION NUMBER: 60/047,614
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EARLIER APPLICATION NUMBER: 60/043,578
EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/043,576
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EARLIER APPLICATION NUMBER: 60/047,501
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/043,670
EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/056,632
EARLIER FILING DATE: 1997-08-22
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EARLIER APPLICATION NUMBER: 60/056,881
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EARLIER APPLICATION NUMBER: 60/056,862
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EARLIER APPLICATION NUMBER: 60/056,887
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,908
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/048,964
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/057,650
EARLIER FILING DATE: 1997-09-05
EARLIER APPLICATION NUMBER: 60/056,884
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/057,669
EARLIER FILING DATE: 1997-09-05
EARLIER APPLICATION NUMBER: 60/049,610
EARLIER FILING DATE: 1997-06-13
EARLIER APPLICATION NUMBER: 60/061,060
EARLIER FILING DATE: 1997-10-02

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Query Match 72.4%; Score 15.2; DB 4; Length 604;
Best Local Similarity 85.0%; Pred. No. 1.2e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
1 AAAGCCCGCATGTCGGG 20

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Db 50 AAAGCCCGCATGTCGGG 31
RESULT 12
US-09-252-991A-4268/c
Sequence 4268, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID SEQUENCES RELATING TO PSEUDOMONAS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
PRIOR FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 4268
LENGTH: 660
TYPE: DNA
ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-4268

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Query Match 72.4%; Score 15.2; DB 4; Length 660;
Best Local Similarity 85.0%; Pred. No. 1.2e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
1 AAAGCCCGCATGTCGGG 20
Db 575 AAAGCCCGCATGTCGGG 556

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RESULT 13
US-09-252-991A-4484
Sequence 4484, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
PRIOR FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 4484
LENGTH: 813
TYPE: DNA
ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-4484

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Query Match 72.4%; Score 15.2; DB 4; Length 813;
Best Local Similarity 85.0%; Pred. No. 1.2e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
1 AAAGCCCGCATGTCGGG 20
Db 18 AAAGCCCGCATGTCGGG 37

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RESULT 14
US-09-252-991A-4200/c
Sequence 4200, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

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/ TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
 / FILE REFERENCE: 107196.136
 / CURRENT APPLICATION NUMBER: US/09/252,991A
 / CURRENT FILING DATE: 1999-02-18
 / PRIOR APPLICATION NUMBER: US 60/074,788
 / PRIOR FILING DATE: 1998-02-18
 / PRIOR APPLICATION NUMBER: US 60/094,190
 / PRIOR FILING DATE: 1998-07-27
 / NUMBER OF SEQ ID NOS: 33142
 / SEQ ID NO 4200
 / LENGTH: 1611
 / TYPE: DNA
 / ORGANISM: Pseudomonas aeruginosa
 US-09-252-991A-4200

Query Match 72.4%; Score 15.2; DB 4; Length 1611;
 Best Local Similarity 85.0%; Pred. No. 1.3e+02;
 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 AAAGCCCGCATGTCGGG 20
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 DB 699 AAAGCCCGCATGTCGGG 680

RESULT 15
 US-09-050-861B-1/c
 / Sequence 1, Application US/09050861B
 / Patent No. 6555314
 / GENERAL INFORMATION:
 / APPLICANT: Payan, Donald
 / TITLE OF INVENTION: TOSO AS A TARGET FOR DRUG SCREENING
 / FILE REFERENCE: RIGL-002CON
 / CURRENT APPLICATION NUMBER: US/09/050,861B
 / CURRENT FILING DATE: 1998-03-30
 / PRIOR APPLICATION NUMBER: US/09/651,150B
 / PRIOR FILING DATE: 2000-08-30
 / PRIOR APPLICATION NUMBER: US 09/050,861
 / PRIOR FILING DATE: 1998-03-30
 / NUMBER OF SEQ ID NOS: 35
 / SOFTWARE: PatentIn version 3.1
 / SEQ ID NO 1
 / LENGTH: 1911
 / TYPE: DNA
 / ORGANISM: Homo sapiens
 US-09-050-861B-1

Query Match 72.4%; Score 15.2; DB 4; Length 1911;
 Best Local Similarity 85.0%; Pred. No. 1.3e+02;
 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 AAAGCCCGCATGTCGGG 20
 |||||
 DB 860 AAAGCCCGCATGTCGGG 841

Search completed: February 12, 2004, 06:07:49
 Job time : 30.6829 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Comphen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 12, 2004, 04:42:03 ; Search time 119.341 Seconds
(without alignments)
648.193 Million cell updates/sec

Title: US-09-692-077d-14

Perfect score: 21
Sequence: 1 aaagcccccacatgctcggt 21

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 2449703 seqs, 1841816367 residues

Total number of hits satisfying chosen parameters: 4899406

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database:

Published Applications NA.*
1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq.*
2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq.*
3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq.*
4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq.*
5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq.*
6: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq.*
7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq.*
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10: /cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq.*
11: /cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq.*
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13: /cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq.*
14: /cgn2_6/ptodata/1/pubpna/US10_PUBCOMB.seq.*
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17: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq.*
18: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	21	100.0	21	US-10-001-073-14	Sequence 14, Appl
2	21	100.0	65	US-09-908-975-4848	Sequence 4848, Ap
3	21	100.0	1344	US-09-825-923-1	Sequence 1, Appl
4	21	100.0	1344	US-10-077-870-1	Sequence 1, Appl
5	21	100.0	1344	US-10-001-073-2	Sequence 2, Appl
6	21	100.0	1353	US-09-825-923-3	Sequence 3, Appl
7	21	100.0	1353	US-10-077-870-3	Sequence 3, Appl
8	21	100.0	1353	US-10-001-073-1	Sequence 1, Appl
9	21	100.0	2072	US-10-305-720-1181	Sequence 1181, Ap
10	21	100.0	3274	US-10-225-567A-41	Sequence 41, Appl
11	16.8	80.0	4350	US-09-814-353-19559	Sequence 19559, A
12	16.4	78.1	481	US-09-918-995-29585	Sequence 29585, A
13	16.4	78.1	565	US-10-027-632-131352	Sequence 131352, A
14	16.4	78.1	565	US-10-027-632-131352	Sequence 131352, A
15	16.4	78.1	2262	US-10-220-891-38	Sequence 38, Appl

16	16.4	78.1	6997	12	US-10-094-886-137	Sequence 137, App
17	16.4	78.1	28438	13	US-09-820-790-3	Sequence 3, Appl
18	16.4	78.1	35178	13	US-10-017-161-739	Sequence 739, App
19	16.2	77.1	607	13	US-10-027-632-139091	Sequence 139091, A
20	16.2	77.1	607	13	US-10-027-632-139092	Sequence 139092, A
21	16.2	77.1	607	13	US-10-027-632-139091	Sequence 139091, A
22	16.2	77.1	607	14	US-10-027-632-139092	Sequence 6, Appl
23	16.2	77.1	1134	15	US-10-084-817-279	Sequence 279, App
24	16.2	77.1	1182	15	US-10-214-519-6	Sequence 6, Appl
25	16.2	77.1	1182	15	US-10-071-338-6	Sequence 6, Appl
26	16.2	77.1	1182	15	US-10-288-985-6	Sequence 6, Appl
27	16.2	77.1	1182	15	US-10-288-985-6	Sequence 6, Appl
28	16.2	77.1	1193	13	US-10-289-980-6	Sequence 1, Appl
29	16.2	77.1	7193	15	US-10-071-338-1	Sequence 1, Appl
30	16.2	77.1	7193	15	US-10-288-985-1	Sequence 1, Appl
31	16.2	77.1	7193	15	US-10-289-980-1	Sequence 1, Appl
32	16	76.2	1446	12	US-10-366-493-27287	Sequence 27287, A
33	15.8	75.2	638	15	US-10-198-846-4384	Sequence 4384, Ap
34	15.8	75.2	716	13	US-10-027-632-25794	Sequence 25794, A
35	15.8	75.2	716	14	US-10-027-632-25794	Sequence 25794, A
36	15.8	75.2	1287	12	US-10-366-493-38571	Sequence 38571, A
37	15.8	75.2	1290	12	US-10-366-493-35369	Sequence 35369, A
38	15.8	75.2	1290	12	US-10-366-493-38026	Sequence 38026, A
39	15.8	75.2	1290	12	US-10-366-493-38181	Sequence 38181, A
40	15.8	75.2	1615	9	US-09-764-860-1074	Sequence 1074, Ap
41	15.8	75.2	1615	13	US-10-212-872-1074	Sequence 1074, Ap
42	15.8	75.2	1615	13	US-10-074-095-1074	Sequence 1074, Ap
43	15.8	75.2	1710	12	US-10-426-776-16	Sequence 16, Appl
44	15.8	75.2	1710	12	US-10-345-660-15	Sequence 15, Appl
45	15.8	75.2	1710	13	US-10-314-881-13	Sequence 13, Appl

ALIGNMENTS

RESULT 1
US-10-001-073-14
; Sequence 14, Application US/10001073
; Publication No. US20030113725A1
; GENERAL INFORMATION:
; APPLICANT: Liggett, Stephen
; APPLICANT: Small, Kirsten
; TITLE OF INVENTION: Alpha-2-adrenergic receptor polymorphisms
; FILE REFERENCE: 13073-PCT
; CURRENT APPLICATION NUMBER: US/10/001, 073
; CURRENT FILING DATE: 2001-11-01
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: Patencin Ver. 2.0
; SEQ ID NO 14
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-001-073-14
Query Match 100.0%; Score 21; DB 15; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DB 1 AAAGCCCCACATGCTCGGCT 21
1 AAAGCCCCACATGCTCGGCT 21
RESULT 2
US-09-908-975-4848/c
; Sequence 4848, Application US/09908975
; Publication No. US20030165843A1
; GENERAL INFORMATION:
; APPLICANT: SHOSHAN, Avi
; APPLICANT: WASSERMAN, Alon
; APPLICANT: MINTZ, Eli
; APPLICANT: MINTZ, Liat
; APPLICANT: FAIGLER, Simchon

TITLE OF INVENTION: OLIGONUCLEOTIDE LIBRARY FOR DETECTING RNA TRANSCRIPTS AND SPLIC
TITLE OF INVENTION: THAT POPULATE A TRANSCRIPTOME
FILE REFERENCE: 36688-0005
CURRENT APPLICATION NUMBER: US/09/908,975
CURRENT FILING DATE: 2001-07-20
PRIOR APPLICATION NUMBER: US 60/287,724
PRIOR FILING DATE: 2001-05-02
PRIOR APPLICATION NUMBER: US 60/221,607
PRIOR FILING DATE: 2000-07-28
NUMBER OF SEQ ID NOS: 32337
SOFTWARE: Patentin version 3.0
SEQ ID NO 4848
LENGTH: 65
TYPE: DNA
ORGANISM: Rattus norvegicus
US-09-908-975-4848

Query Match 100.0%; Score 21; DB 13; Length 65;
Best Local Similarity 100.0%; Pred. No. 1.7;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAAGCCCAACCATGTCGGGT 21
DB 45 AAAGCCCAACCATGTCGGGT 25

RESULT 3
US-09-825-923-1/c
Sequence 1, Application US/09825923
Patent No. US20010016338A1
GENERAL INFORMATION:
APPLICANT: Snapir, Amir
APPLICANT: Heinonen, Paula
APPLICANT: Alhopuro, Pia
APPLICANT: Karvonen, Matti
APPLICANT: Koulu, Markku
APPLICANT: Pesonen, Ullamari
APPLICANT: Scheinin, Mika
APPLICANT: Salonen, Jukka T
APPLICANT: Tuomala, Tomi-Pekka
APPLICANT: Lakkas, Timo A
APPLICANT: Nyysanen, Kristina
APPLICANT: Salonen, Riitta
APPLICANT: Kaubanen, Jussi
APPLICANT: Valonen, Veli-Pekka
TITLE OF INVENTION: A DNA molecule encoding a variant alpha-2B-adrenoceptor
FILE REFERENCE: Protein, and uses thereof
CURRENT APPLICATION NUMBER: US/09/825,923
CURRENT FILING DATE: 2001-04-05
PRIOR APPLICATION NUMBER: 09/422,985
PRIOR FILING DATE: 2000-05-25
NUMBER OF SEQ ID NOS: 10
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 1
LENGTH: 1344
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (1)..(1341)
OTHER INFORMATION: Coding sequence for variant human
OTHER INFORMATION: alpha-2B-adrenoceptor protein
US-09-825-923-1

Query Match 100.0%; Score 21; DB 9; Length 1344;
Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAAGCCCAACCATGTCGGGT 21
DB 686 AAAGCCCAACCATGTCGGGT 666

RESULT 4
US-10-077-870-1/c
Sequence 1, Application US/10077870
Publication No. US2003003470A1
GENERAL INFORMATION:
APPLICANT: Salonen, Jukka T
TITLE OF INVENTION: Method for detecting a risk of hypertension and uses thereof
FILE REFERENCE: 0933-0183P
CURRENT APPLICATION NUMBER: US/10/077,870
CURRENT FILING DATE: 2002-05-21
PRIOR APPLICATION NUMBER: FI 20010323
PRIOR FILING DATE: 2001-02-20
NUMBER OF SEQ ID NOS: 10
SOFTWARE: Patentin Ver. 3.1
SEQ ID NO 1
LENGTH: 1344
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (1)..(1341)
OTHER INFORMATION: Coding sequence for variant human alpha-2B-adrenoceptor protein
US-10-077-870-1

Query Match 100.0%; Score 21; DB 15; Length 1344;
Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAAGCCCAACCATGTCGGGT 21
DB 686 AAAGCCCAACCATGTCGGGT 666

RESULT 5
US-10-001-073-2/c
Sequence 2, Application US/10001073
Publication No. US20030113725A1
GENERAL INFORMATION:
APPLICANT: Liggett, Stephen
APPLICANT: Small, Kirsten
TITLE OF INVENTION: Alpha-2-adrenergic receptor polymorphisms
FILE REFERENCE: 13073-BCT
CURRENT APPLICATION NUMBER: US/10/001,073
CURRENT FILING DATE: 2001-11-01
NUMBER OF SEQ ID NOS: 53
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 2
LENGTH: 1344
TYPE: DNA
ORGANISM: Homo sapiens
US-10-001-073-2

Query Match 100.0%; Score 21; DB 15; Length 1344;
Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAAGCCCAACCATGTCGGGT 21
DB 686 AAAGCCCAACCATGTCGGGT 666

RESULT 6
US-09-825-923-3/c
Sequence 3, Application US/09825923
Patent No. US20010016338A1
GENERAL INFORMATION:
APPLICANT: Snapir, Amir
APPLICANT: Heinonen, Paula
APPLICANT: Alhopuro, Pia
APPLICANT: Karvonen, Matti
APPLICANT: Koulu, Markku
APPLICANT: Pesonen, Ullamari

APPLICANT: Scheinin, Mika
APPLICANT: Salonen, Jukka T
APPLICANT: Tuominen, Tomi-Pekka
APPLICANT: Lakka, Timo A
APPLICANT: Myrskylä, Kristina
APPLICANT: Salonen, Riitta
APPLICANT: Kauppinen, Jussi
APPLICANT: Valonen, Veli-Pekka
TITLE OF INVENTION: A DNA molecule encoding a variant alpha-2B-adrenoceptor
FILE REFERENCE: Alpha-2B-AR variant
CURRENT APPLICATION NUMBER: US/09/825,923
PRIORITY FILING DATE: 2001-04-05
PRIORITY APPLICATION NUMBER: 09/422,985
PRIORITY FILING DATE: 2000-05-25
NUMBER OF SEQ ID NOS: 10
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 3
LENGTH: 1353
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (1)..(1350)
OTHER INFORMATION: Coding sequence for human alpha-2B-adrenoceptor
US-09-825-923-3

Query Match 100.0%; Score 21; DB 9; Length 1353;
Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 AAAGCCCAACCATGTCGGGT 21
Db 686 AAAGCCCAACCATGTCGGGT 666

RESULT 7
US-10-077-870-3/C
Sequence 3, Application US/10077870
Publication No. US20030003470A1
GENERAL INFORMATION:
APPLICANT: Salonen, Jukka T
TITLE OF INVENTION: Method for detecting a risk of hypertension and uses thereof
FILE REFERENCE: 0933-0183P
CURRENT FILING DATE: 2002-05-21
CURRENT APPLICATION NUMBER: US/10/077,870
PRIORITY FILING DATE: 2001-02-20
PRIORITY APPLICATION NUMBER: FI 20010323
NUMBER OF SEQ ID NOS: 10
SOFTWARE: Patentin Ver. 3.1
SEQ ID NO 3
LENGTH: 1353
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (1)..(1350)
OTHER INFORMATION: Coding sequence for human alpha-2B-adrenoceptor protein
US-10-077-870-3

Query Match 100.0%; Score 21; DB 15; Length 1353;
Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 AAAGCCCAACCATGTCGGGT 21
Db 686 AAAGCCCAACCATGTCGGGT 666

RESULT 8
US-10-001-073-1/C
Sequence 1, Application US/10001073

Publication No. US20030113725A1
GENERAL INFORMATION:
APPLICANT: Liggett, Stephen
APPLICANT: Small, Kirsten
TITLE OF INVENTION: Alpha-2-adrenergic receptor polymorphisms
FILE REFERENCE: 13073-PCT
CURRENT APPLICATION NUMBER: US/10/001,073
PRIORITY FILING DATE: 2001-11-01
NUMBER OF SEQ ID NOS: 53
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1
LENGTH: 1353
TYPE: DNA
ORGANISM: Homo sapiens
US-10-001-073-1

Query Match 100.0%; Score 21; DB 15; Length 1353;
Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 AAAGCCCAACCATGTCGGGT 21
Db 686 AAAGCCCAACCATGTCGGGT 666

RESULT 9
US-10-305-720-1181/C
Sequence 1181, Application US/10305720
Publication No. US20040010136A1
GENERAL INFORMATION:
APPLICANT: Au-Young, Janice K.; Seilhamer, Jeffrey J.
TITLE OF INVENTION: Composition for the Detection of Signaling Pathway Gene Expression
FILE REFERENCE: PA-0002-1 CON
CURRENT FILING DATE: 2002-11-26
CURRENT APPLICATION NUMBER: US/10/305,720
PRIORITY FILING DATE: 1998-01-30
PRIORITY APPLICATION NUMBER: 09/016,434
NUMBER OF SEQ ID NOS: 1490
SOFTWARE: PERL Program
SEQ ID NO 1181
LENGTH: 2072
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
OTHER INFORMATION: GenBank ID No. US20040010136A1 G178197
US-10-305-720-1181

Query Match 100.0%; Score 21; DB 12; Length 2072;
Best Local Similarity 100.0%; Pred. No. 1.3;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 AAAGCCCAACCATGTCGGGT 21
Db 1098 AAAGCCCAACCATGTCGGGT 1078

RESULT 10
US-10-225-567A-41/C
Sequence 41, Application US/10225567A
Publication No. US20030113798A1
GENERAL INFORMATION:
APPLICANT: Lifespan Biosciences
APPLICANT: Brown, Joseph P.
APPLICANT: Burner, Glenn C.
APPLICANT: Roush, Christine L.
TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS
FILE REFERENCE: 1920-4-4
CURRENT APPLICATION NUMBER: US/10/225,567A
PRIORITY FILING DATE: 2001-12-19
PRIORITY APPLICATION NUMBER: 60/257,144
PRIORITY FILING DATE: 2000-12-19
NUMBER OF SEQ ID NOS: 2292

SOFTWARE: PatentIn version 3.1
SEQ ID NO 41
LENGTH: 3274
TYPE: DNA
ORGANISM: Homo sapiens
US-10-225-567A-41

Query Match 100.0%; Score 21; DB 15; Length 3274;
Best Local Similarity 100.0%; Pred. No. 1.3;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAGCCCCACATGCTCGGGT 21
DB 686 AAGCCCCACATGCTCGGGT 666

RESULT 11
US-09-814-353-19559
Sequence 19559, Application US/09814353
Publication No. US20030165831A1
GENERAL INFORMATION:
APPLICANT: Lee, John
APPLICANT: Thompson, Pamela
APPLICANT: Illie, James
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
IDENTIFICATION, ASSESSMENT, PREVENTION, AND
THERAPY OF OVARIAN CANCER
FILE REFERENCE: MRI-006B
CURRENT APPLICATION NUMBER: US/09/814,353
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: US 60/191,031
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: US 60/207,124
PRIOR FILING DATE: 2000-05-25
PRIOR APPLICATION NUMBER: US 60/211,940
PRIOR FILING DATE: 2000-06-15
PRIOR APPLICATION NUMBER: US 60/216,820
PRIOR FILING DATE: 2000-07-07
PRIOR APPLICATION NUMBER: US 60/220,661
PRIOR FILING DATE: 2000-07-25
PRIOR APPLICATION NUMBER: US 60/257,672
PRIOR FILING DATE: 2000-12-21
NUMBER OF SEQ ID NOS: 22037
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 19559
LENGTH: 4350
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: 4327..4328, 4339, 4331, 4332, 4333, 4334, 4335, 4336,
LOCATION: 4337, 4338, 4339, 4340, 4341, 4342, 4343, 4344, 4345, 4346,
LOCATION: 4347, 4348, 4349, 4350
OTHER INFORMATION: n = A,T,C or G
US-09-814-353-19559

Query Match 80.0%; Score 16.8; DB 13; Length 4350;
Best Local Similarity 90.0%; Pred. No. 1.3e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 AAGCCCCACATGCTCGGG 20
DB 3482 AAGCCCCACATGCTCGGG 3501

RESULT 12
US-09-918-995-29585/c
Sequence 29585, Application US/09918995
Publication No. US20030073623A1
GENERAL INFORMATION:
APPLICANT: HySeq, Inc.
TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
FROM VARIOUS CDNA LIBRARIES

FILE REFERENCE: 20411-756
CURRENT APPLICATION NUMBER: US/09/918,995
CURRENT FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: US/09/235,076
PRIOR FILING DATE: 1999-01-20
NUMBER OF SEQ ID NOS: 38054
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 29585
LENGTH: 481
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(481)
OTHER INFORMATION: n = A,T,C or G
US-09-918-995-29585

Query Match 78.1%; Score 16.4; DB 11; Length 481;
Best Local Similarity 94.4%; Pred. No. 2.3e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 AGCCCCACATGCTCGGG 20
DB 394 AGCCCCACATGCTCGGG 377

RESULT 13
US-10-027-632-131352/c
Sequence 131352, Application US/10027632
Publication No. US20030204075A9
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
Polymorphisms in the Human Genome
FILE REFERENCE: 108827.129
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR FILING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR FILING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR FILING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 131352
LENGTH: 565
TYPE: DNA
ORGANISM: Human
US-10-027-632-131352

Query Match 78.1%; Score 16.4; DB 13; Length 565;
Best Local Similarity 94.4%; Pred. No. 2.3e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 AGCCCCACATGCTCGGG 20
DB 551 AGCCCCACATGCTCGGG 534

RESULT 14
US-10-027-632-131352/c
Sequence 131352, Application US/10027632
GENERAL INFORMATION:
APPLICANT: Wang, David G.

TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
FILE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108827.129
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR FILING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR FILING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR FILING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 131352
LENGTH: 565
TYPE: DNA
ORGANISM: Human
US-10-027-632-131352

Query Match 78.1%; Score 16.4; DB 13; Length 565;
Best Local Similarity 94.4%; Pred. No. 2.3e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 AGCCCCACCATGTCGGG 20
|||||
DB 551 AGCCCCACCATGTCGGG 534

RESULT 15
US-10-220-891-38/c
Sequence 38, Application US/10220891
Publication No. US20030207286A1
GENERAL INFORMATION:
APPLICANT: NAKAGAWA, AKIRA
TITLE OF INVENTION: NUCLEIC ACID SEQUENCES HAVING CHARACTERISTICS OF ENHANCED
TITLE OF INVENTION: EXPRESSION IN HUMAN NEUROBLASTOMA WITH FAVORABLE PROGNOSIS
TITLE OF INVENTION: BASED ON COMPARISON BETWEEN HUMAN NEUROBLASTOMA WITH FAVORABLE
TITLE OF INVENTION: PROGNOSIS AND HUMAN NEUROBLASTOMA WITH UNFAVORABLE PROGNOSIS
FILE REFERENCE: 7386-73435
CURRENT APPLICATION NUMBER: US/10/220,891
CURRENT FILING DATE: 2003-03-07
PRIOR APPLICATION NUMBER: JP 2000/140387
PRIOR FILING DATE: 2000-05-12
PRIOR APPLICATION NUMBER: JP 2000/159195
PRIOR FILING DATE: 2000-03-07
NUMBER OF SEQ ID NOS: 108
SOFTWARE: PatentIn version 3.2
SEQ ID NO 38
LENGTH: 2262
TYPE: DNA
ORGANISM: Homo sapiens
US-10-220-891-38

Query Match 78.1%; Score 16.4; DB 13; Length 2262;
Best Local Similarity 94.4%; Pred. No. 2.1e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 AGCCCCACCATGTCGGG 20
|||||
DB 1487 AGCCCCACCATGTCGGG 1470

Search completed: February 12, 2004, 06:15:44
Job time : 128.341 secs

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OM nucleic - nucleic search, using sw model

Run on: February 12, 2004, 03:54:41 ; Search time 1135.79 Seconds
(without alignments)
449.373 Million cell updates/sec

Title: US-09-692-077D-14

Perfect score: 21
Sequence: 1 aaagcccccacatgctcg9gc 21

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 22781392 seqs, 12152238056 residues

Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Selecting first 45 summaries

Database :

EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estnu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_hic:*
9: gb_est1:*
10: gb_est2:*
11: gb_hic:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: em_gse_hum:*
18: em_gse_hiv:*
19: em_gse_pln:*
20: em_gse_vrt:*
21: em_gse_fun:*
22: em_gse_mam:*
23: em_gse_mus:*
24: em_gse_pro:*
25: em_gse_rtd:*
26: em_gse_pbg:*
27: em_gse_vrl:*
28: gb_gse1:*
29: gb_gse2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	21	100.0	1044	13	BQ880026
2	18.4	87.6	261	9	AW391095
3	17.8	84.8	269	9	AW582395
4	17.8	84.8	376	9	AW166948

5	17.8	84.8	724	9	AI19320	AI19320 tef2e11.x
6	17.8	84.8	921	9	AL56668	AL56668 AL56668
7	17.8	84.8	956	13	BQ923897	BQ923897 AGENCOURT
8	17.4	82.9	212	9	AI216547	AI216547 cm36h04.x
9	17.4	82.9	487	9	AI869725	AI869725 w198h12.x
10	17.4	82.9	740	28	BH794919	BH794919 ME_MBA000
11	17.4	82.9	1485	28	BI687242	BI687242 603314820
12	17.4	82.9	666	12	A2571445	A2571445 287PVG04
13	17.4	82.9	903	12	BP111519	BP111519 BP111519
14	17.4	82.9	760	12	BM469354	BM469354 AGENCOURT
15	17.4	82.9	1017	12	BQ053165	BQ053165 AGENCOURT
16	16.8	80.0	376	13	BY401935	BY401935 BY401935
17	16.8	80.0	407	13	BX316223	BX316223 BX316223
18	16.8	80.0	449	9	AI494022	AI494022 q297h04.x
19	16.8	80.0	492	14	CA912228	CA912228 PCSC21166
20	16.8	80.0	659	9	AM161813	AM161813 au70604.x
21	16.8	80.0	697	14	CB529586	CB529586 UI-H-FT2-
22	16.8	80.0	726	28	BH794448	BH794448 ME_MBA000
23	16.8	80.0	894	29	CNS031RL	AL223914 Tetradon
24	16.8	80.0	896	13	BQ603088	BQ603088 AGENCOURT
25	16.8	80.0	912	10	BF307809	BF307809 601890896
26	16.8	80.0	946	9	AL549851	AL549851 AL549851
27	16.8	80.0	950	9	AL533975	AL533975 AL533975
28	16.8	80.0	957	29	BZ551182	BZ551182 pacer1-60
29	16.8	80.0	1029	12	BQ061158	BQ061158 AGENCOURT
30	16.8	80.0	1059	13	BUS87459	BUS87459 AGENCOURT
31	16.8	80.0	1146	10	BG242458	BG242458 602354253
32	16.4	78.1	212	10	BR946030	BR946030 CM0-NN115
33	16.4	78.1	333	13	BF811542	BF811542 CM2-C1017
34	16.4	78.1	333	13	BY149362	BY149362 BY149362
35	16.4	78.1	341	13	BY195012	BY195012 BY195012
36	16.4	78.1	345	13	BY214037	BY214037 BY214037
37	16.4	78.1	354	13	BY337375	BY337375 BY337375
38	16.4	78.1	360	13	BY200267	BY200267 BY200267
39	16.4	78.1	365	14	CB069817	CB069817 1829e01.Y
40	16.4	78.1	379	9	AA448022	AA448022 zw97b03.Y
41	16.4	78.1	430	10	BE517145	BE517145 WHE0624.F
42	16.4	78.1	433	9	AA448451	AA448451 zw96h03.Y
43	16.4	78.1	442	9	AA447622	AA447622 zw97b03.B
44	16.4	78.1	446	12	BI713098	BI713098 ie02b10.Y
45	16.4	78.1	448	9	AA448314	AA448314 zw96h03.B

ALIGNMENTS

RESULT 1
LOCUS BQ880026/c 1044 bp mRNA linear EST 16-AUG-2002
DEFINITION AGENCOURT 8113358 lupski dorsal_root_ganglion Homo sapiens cDNA
clone IMAGE:6179035 5', mRNA sequence.
ACCESSION BQ880026
VERSION BQ880026.1 GI:22272034
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE NIH-MGC http://mgs.nci.nih.gov/.
AUTHORS Mammalia; Eutheria; Primates; Carnivora; Hominoidea; Homo.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgaabbs-r@mail.nih.gov
Tissue Procurement: Dr. James R. Lupski
CDNA Library Preparation: Life Technologies, Inc.
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: L1AM13559 row: 1 column: 20
High quality sequence stop: 430.

FEATURES
source

Location/Qualifiers
1. 1044
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6179035"
/sex="male"
/tissue_type="dorsal root ganglia"
/dev_stage="adult, 36 yr"
/lab_host="DH10B"
/clone_lib="Lupski dorsal root ganglion"
/note="Vector: PCMV-SPORT6 (Life Technologies); Site 1: NotI; Site 2: SalI; cDNA made by oligo-dT priming. Directionally cloned using the following adaptors: 5'-TCGACCCGACCGTCGCG-3' and 5'-GACGAGTTTGTAGTCGACGCGCCCT(15)-3'. Size selected > 1 kb for average insert length 1.7 kb. This is a primary library, non-amplified. Library constructed by Life Technologies and donated by J. Lupski, M.D./Ph.D. (Baylor College of Medicine) and is available through Life Technologies."

BASE COUNT
182 a 334 c 345 g 183 t

ORIGIN

Query Match
Best Local Similarity 100.0%; Score 21; DB 13; Length 1044;
Pred. No. 29;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY
1 AAAGCCCCACCATGTCGGGT 21
|||||
223 AAAGCCCCACCATGTCGGGT 203
|||||

RESULT 2
AM391095 261 bp mRNA linear EST 04-FEB-2000
LOCUS MR3-ST0203-131299-111-F11 ST0203 Homo sapiens cDNA, mRNA sequence.
DEFINITION
ACCESSION AM391095
VERSION AM391095.1 GI:6895754
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 261)
HGCP http://www.ludwig.org.br/ORESTES.
The FAPESP/LICR Human Cancer Genome Project
Unpublished
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?l=MR3&t2=MR3-ST0203-131299-111-F11&t3=1999-12-13&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 10
High quality sequence stop: 63.
Location/Qualifiers
1. 261
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_lib="ST0203"
/note="Organ: stomach; Vector: puc18; Site 1: SmaI; Site 2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application

FEATURES
source

No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

BASE COUNT
67 a 54 c 80 g 60 t

ORIGIN

Query Match
Best Local Similarity 95.0%; Score 18.4; DB 9; Length 261;
Pred. No. 3.6e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY
2 AAGCCCCACCATGTCGGGT 21
|||||
54 AAGCCCCACCATGTCGGGT 73
|||||

RESULT 3
A1582395 269 bp mRNA linear EST 14-DEC-1999
LOCUS U197b09.x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2227001 3',
DEFINITION
ACCESSION A1582395
VERSION A1582395
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 269)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
Unpublished
Contact: Robert Strausberg, Ph.D.
Email: cgabs-r@mail.nih.gov
Life Technologies catalog #: 11548-013
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/ILIN at:
www.bio.liln.gov/bdir/image/image.html
Insert Length: 1875 Std Error: 0.00
Seq primer: -40UP from G1bco
High quality sequence stop: 141
POLYA=No.

FEATURES
source

Location/Qualifiers
1. 269
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2227001"
/tissue_type="adenocarcinoma"
/lab_host="DH10B"
/clone_lib="NCI_CGAP_Pan1"
/note="Organ: pancreas; Vector: PCMV-SPORT6; Site 1: SalI; Site 2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.72 kb. Life Technologies catalog #:
11548-013"

BASE COUNT
80 a 44 c 49 g 96 t

ORIGIN

Query Match
Best Local Similarity 84.8%; Score 17.8; DB 9; Length 269;
Pred. No. 6.9e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY
1 AAAGCCCCACCATGTCGGGT 21
|||||
209 AAGCCCCACCATGTCGGGT 229
|||||

RESULT 4
AUI66948 376 bp mRNA linear EST 03-APR-2002
LOCUS AUI66948
DEFINITION AUI66948 Rice callus (2001) Oryza sativa (japonica cultivar-group)

ACCESSION CDNA clone C60162, mRNA sequence.
 VERSION AU166948
 KEYWORDS AU166948.1 GI:12405347
 SOURCE EST.
 ORGANISM Oryza sativa (japonica cultivar-group)
 Oryza sativa (japonica cultivar-group)
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Ehrhacridae; Oryzaceae; Oryza.
 1 (bases 1 to 376)
 Sasaki, T. and Yamamoto, K.
 Rice cDNA from callus (2001)
 Unpublished
 Contact: Takuji Sasaki
 National Institute of Agrobiological Resources
 Rice Genome Research Program, Kannondai 2-1-2, Tsukuba, Ibaraki
 305-8602, Japan
 Tel: 81-298-38-7441
 Fax: 81-298-38-7468
 Email: tsasaki@abrr.affrc.go.jp, URL: http://rgp.dna.affrc.go.jp/
 PROJECT "RGP".
 FEATURES
 source location/Qualifiers
 1..376
 /organism="Oryza sativa (japonica cultivar-group)"
 /mol_type="mRNA"
 /cultivar="Nipponbare"
 /db_xref="taxon:39947"
 /clone="C60162"
 /tissue_type="callus"
 /clone_lib="Rice callus (2001)"
 BASE COUNT 102 a 81 c 81 g 106 t 6 others
 ORIGIN
 Query Match 84.8%; Score 17.8; DB 9; Length 376;
 Best Local Similarity 90.5%; Pred. No. 7.2e+02;
 Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 Oy 1 AAAGCCCAACATGTCGGGT 21
 Db 132 AATGCCCAACATGTCGGGT 112
 RESULT 5 724 bp mRNA linear EST 30-MAR-1999
 A1419320
 LOCUS t272ell.x1 NCI CGAP Brn23 Homo sapiens cDNA clone IMAGE:2097452 3'
 DEFINITION similar to gb:X52255_tma1 CYSSTATIN C PRECURSOR (HUMAN);, mRNA
 sequence.
 ACCESSION A1419320
 VERSION A1419320
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homindae; Homo.
 1 (bases 1 to 724)
 NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap
 National Cancer Institute / National Institute of Neurological
 Disorders and Stroke, Brain Tumor Genome Anatomy Project
 (CGAP/BrGAP), Tumor Gene Index
 Unpublished
 Contact: Robert Strausberg, Ph.D.
 Email: cga@bbs-r@mail.nih.gov
 Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D.,
 Ph.D.
 cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
 Bonaldo, Ph.D.
 cDNA Library Arrayed by: Greg Lennon, Ph.D.
 DNA Sequencing by: Washington University Genome Sequencing Center
 Clone distribution: NCI-CGAP clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 www-bio.llnl.gov/bbrp/image/image.html
 Insert length: 835 Std Error: 0.00

Seq primer: -40UP from Gibco
 High quality sequence stop: 412.
 FEATURES
 source location/Qualifiers
 1..724
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:2097452"
 /tissue_type="glioblastoma (pooled)"
 /lab_host="DH10B"
 /clone_lib="NCI CGAP Brn23"
 /note="Organ: Brain; Vector: pT7T3D-Pec (Pharmacia) with a
 modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st
 strand cDNA was primed with a Not I - oligo(dT) primer [5'
 TGTTCACATCTGAGTGAGCGCCCATCTCTTTTCTTTTCTTTTCTTTTCTTTT
 T 3']; double-stranded cDNA was ligated to Eco RI
 adaptors (Pharmacia), digested with Not I and cloned into
 the Not I and Eco RI sites of the modified pT7T3 vector.
 Library is normalized, and was constructed by Bento
 Soares and M. Fatima Bonaldo."
 BASE COUNT 141 a 204 c 242 g 134 t 3 others
 ORIGIN
 Query Match 84.8%; Score 17.8; DB 9; Length 724;
 Best Local Similarity 90.5%; Pred. No. 8e+02;
 Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 Oy 1 AAAGCCCAACATGTCGGGT 21
 Db 682 AAAGCCCAACATGTCGGGT 702
 RESULT 6 921 bp mRNA linear EST 31-MAY-2003
 AL566688
 LOCUS AL566688 Homo sapiens FETAL BRAIN Homo sapiens cDNA clone
 DEFINITION CSODP019YH12 3-PRIME, mRNA sequence.
 ACCESSION AL566688
 VERSION AL566688
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homindae; Homo.
 1 (bases 1 to 921)
 Li, W.B., Gruber, C., Jesse, J. and Polayes, D.
 Full-length cDNA libraries and normalization
 Unpublished
 On Feb 16, 2001 this sequence version replaced gi:12919302.
 Contact: Genoscope
 Genoscope - Centre National de Sequencage
 BP 191 91006 EVRY cedex - France
 Email: segre@genoscope.cns.fr, Web: www.genoscope.cns.fr
 Library was constructed by life technologies, a division of
 Invitrogen. This sequence belongs to sequence cluster 8536.r For
 more information about this cluster, see
 http://www.genoscope.cns.fr/
 cgi-bin/cluster.cgi?seq=CSODP019DD06NP1c1uster=8536.r. Contact :
 Feng Liang Email : fliang@life.techn.com URL :
 http://fulllength.invitrogen.com/ invitrogen Corporation 1600
 Faraday Avenue Genoscope sequence ID : CSODP019DD06NP1.
 FEATURES
 source location/Qualifiers
 1..921
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="CSODP019YH12"
 /tissue_type="FETAL BRAIN"
 /dev_stage="fetal"
 /clone_lib="Homo sapiens FETAL BRAIN"
 /note="Organ: brain; Vector: pCMVSPORT_6; 1st strand cDNA
 was primed with a NciI-oligo(dT) primer. Five prime end
 enriched, double-strand cDNA was digested with Not I and

cloned into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library was not normalized."

BASE COUNT 231 a 184 c 269 g 176 t 61 others

ORIGIN

Query Match 84.8%; Score 17.8; DB 9; Length 921;
Best Local Similarity 90.5%; Pred. No. 8.3e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 AAAGCCCAACATGTCGGGT 21
|||||
Db 544 AAAGCCCAACATGTCGGGT 564

RESULT 7
BQ923897/c 956 bp mRNA linear EST 20-AUG-2002
LOCUS AGENCOURT_8854334 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:6473613
DEFINITION 5', mRNA sequence.
ACCESSION BQ923897
VERSION BQ923897.1 GI:22338928
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
NIH-MGC <http://mgc.nci.nih.gov/>.
1 (bases 1 to 956)
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished
Contact: Robert Strausberg, Ph.D.
Email: cgabbs-remail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Life Technologies, Inc.
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: <http://image.llnl.gov>
Plate: LLM14009 row: g column: 22
High quality sequence stop: 413.
Location/Qualifiers
1..956
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6473613"
/tissue_type="leiomyosarcoma"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH MGC 71"
/note="Organ: uterus; Vector: pCMV-SPORT6; Site 1: NotI; Site 2: SalI; Cloned unidirectionally. Primer: Oligo dt. Average insert size 2.1 Kb."
BASE COUNT 247 a 248 c 228 g 233 t

Query Match 84.8%; Score 17.8; DB 13; Length 956;
Best Local Similarity 90.5%; Pred. No. 8.4e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 AAAGCCCAACATGTCGGGT 21
|||||
Db 936 AAAGCCCAACATGTCGGGT 916

RESULT 8
AI216547/c 212 bp mRNA linear EST 02-DEC-1998
LOCUS CM36H04.X1 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1883959 3',
DEFINITION mRNA sequence.
ACCESSION AI216547
VERSION AI216547.1 GI:3785588
KEYWORDS EST.

SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 212)
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
JOURNAL Unpublished
CONTACT: Robert Strausberg, Ph.D.
Email: cgabbs-remail.nih.gov
Tissue Procurement: Christopher Moskalko, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: www.bio.llnl.gov/bbrp/image/image.html
Insert Length: 589 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 177.
Location/Qualifiers
1..212
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:1883959"
/tissue_type="carcinoid"
/lab_host="DH10B"
/clone_lib="NCI_CGAP_Lu5"
/note="Organ: lung; Vector: p7T3D-Pac (pharmacia) with a modified polylinker; 1st strand cDNA was prepared from a neuroendocrine lung carcinoid, and was then primed with a Not I - oligo(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptor (pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified p7T3 vector. Library is normalized. Library was constructed by Bento Soares and M. Fatima Bonaldo."

BASE COUNT 53 a 51 c 60 g 48 t

ORIGIN

Query Match 82.9%; Score 17.4; DB 9; Length 212;
Best Local Similarity 94.7%; Pred. No. 1e+03; 1; Indels 0; Gaps 0;
Matches 18; Conservative 0; Mismatches 1;

QY 1 AAAGCCCAACATGTCGG 19
|||||
Db 104 AAAGCCCAACATGTCGG 86

RESULT 9
AI869725/c 487 bp mRNA linear EST 07-MAR-2000
LOCUS w198h12.x1 NCI CGAP Brn25 Homo sapiens cDNA clone IMAGE:2432999 3',
DEFINITION similar to gb:U11285 DUAL SPECIFICITY MITOGEN-ACTIVATED PROTEIN KINASE KINASE 2 (HUMAN);, mRNA sequence.
ACCESSION AI869725
VERSION AI869725.1 GI:5543693
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 487)
NCI/NINDS-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
TITLE National Cancer Institute / National Institute of Neurological Disorders and Stroke, Brain Tumor Genome Anatomy Project (CGAP/BRGAP), Tumor Gene Index
JOURNAL Unpublished
CONTACT: Robert Strausberg, Ph.D.
Email: cgabbs-remail.nih.gov
Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D.,

Best Local Similarity 94.7%; Pred. No. 1.4e+03;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AAAGCCCAACCATGTCG 19
Db 1404 AAAGCCCAACCATGTCG 1422

RESULT 12
AZ571445/c 696 bp DNA linear GSS 15-MAY-2001
LOCUS 287Pc04 Pv MBN #30 Plasmodium vivax genomic 3', genomic survey
DEFINITION

ACCESSION AZ571445
VERSION AZ571445.1 GI:13983537
KEYWORDS GSS.
SOURCE Plasmodium vivax (malaria parasite P. vivax)
ORGANISM Plasmodium vivax
Eukaryota; Alveolata; Apicomplexa; Haemosporidia; Plasmodium.

REFERENCE 1 (bases 1 to 696)
AUTHORS Carlton, J.M.-R. and Dame, J.B.
TITLE The Plasmodium vivax and P. berghoi gene sequence tag projects
JOURNAL Parasitol. Today (Regul. Ed.) 16 (10), 409 (2000)
COMMENT Contact: Dame JB
Dept. of Pathobiology, College of Veterinary Medicine
University of Florida
2015 SW 23rd Avenue, Bldg 1017, Gainesville, FL 32611, USA
Tel: 352 392 4700
Fax: 352 392 9704
Email: damej@mail.ufl.edu
Seq primer: M13(-20) Forward
Class: Shotgun.

FEATURES
source
1..696
Location/Qualifiers

/organism="Plasmodium vivax"
/mol_type="genomic DNA"
/strain="Salvador I (Collins, W. 1972. J. Parasitol. 69,
497-598)"
/db_xref="taxon:5855"
/dev_stage="asexual blood forms"
/lab_host="Salimiri boliviensis"
/clone_lib="PV MBN #30"
/note="Vector: Bluescript SK(+) vector DNA, phagemid
excised from lambda ZAP; Site 1: EcoR V; Site 2: EcoR V;
Host leukocytes were extracted from P. vivax infected
blood using the following methods: first, infected blood
was activated by the addition of 0.5 ml of ADP (40mg/ml)
per 10 ml blood. Then blood was passed over a column of
acid washed 0.1 mm glass beads, then through a Plasmidipur
filter, followed by passage through a column of pre-wet
Whatman CRI1 powder (1:2 ratio volume of blood to CRI1),
and finally centrifuged through a 50% percoll density
cushion. Purified DNA was digested with mung bean nuclease
in the presence of 4% formamide at 500C as described
(Vernick, K.D., Imberiski, R.B., and McCutchan, T.F. 1988.
Nucleic Acids Research 16:6883-6896). Digested DNA was
blunt-ended using T4 DNA Polymerase and size fractionated
over a Sepharose CL-2B column. Fractions in the size range
500bp-4kb were ligated into the Eco RV site of pBluescript
SK(+), and E. coli XL-10 Gold transformed with the
ligation mixture."

BASE COUNT 181 a 198 c 185 g 126 t 6 others
ORIGIN

Query Match 81.0%; Score 17; DB 28; Length 696;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAAGCCCAACCATGTC 17
Db 696 AAAGCCCAACCATGTC 680

RESULT 13
BP111519/c 703 bp mRNA linear EST 11-FEB-2003
LOCUS BP111519 ORCS bovine utero-placenta cDNA Bos taurus cDNA clone
DEFINITION ORCS11942 5', mRNA sequence.

ACCESSION BP111519
VERSION BP111519.1 GI:28313809
KEYWORDS EST.
SOURCE Bos taurus (cow)
ORGANISM Bos taurus (cow)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovidae; Bovinae; Bos.

REFERENCE 1 (bases 1 to 703)
AUTHORS Iehiwa, H., Katsuna, S., Kizaki, K., Patel, O.V., Nakano, H.,
Takahashi, T., Imai, K., Hirasawa, A., Shiojima, S., Ikawa, H., Suzuki,
Y., Tsujimoto, G., Izaika, Y., Todoroki, J. and Hashizume, K.
TITLE Characterization of gene expression profiles in early bovine
pregnancy using a custom cDNA microarray

JOURNAL Mol. Reprod. Dev. 65 (1), 9-18 (2003)
MEDLINE 22544902
PMID 12658628
COMMENT Contact: Gozoh Tsujimoto
Department of Molecular, Cell Pharmacology
National Research Institute for Child Health and Development
3-35-31 Taitshido, Setagaya, Tokyo 154-8567, Japan
Tel: 81-3-3149-2476
Fax: 81-3-3149-1252
Email: gtsujimoto@nch.go.jp

This work was performed to collaborate with Developmental Biology
Department, National Institute of Agrobiological Sciences. Address:
2 Ikendai, Tsukuba, Ibaraki, 305-8602 Japan. Phone & Fax:
81-29-838-8635 e-mail: kazuhisa@nri.go.jp
This work was funded by Organized Research Combination System (ORCS
) project of Ministry of Education, Culture, Sports, Science and
Technology.

FEATURES
source
1..703
Location/Qualifiers

/organism="Bos taurus"
/mol_type="mRNA"
/db_xref="taxon:9913"
/clone_lib="ORCS11942"
/tissue_type="mixture of uterus and placenta"
/dev_stage="adult"
/clone_lib="ORCS bovine utero-placenta cDNA"

BASE COUNT 163 a 152 c 203 g 183 t 2 others
ORIGIN

Query Match 81.0%; Score 17; DB 12; Length 703;
Best Local Similarity 100.0%; Pred. No. 1.9e+03;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAAGCCCAACCATGTC 17
Db 166 AAAGCCCAACCATGTC 150

RESULT 14
BM469354/c 960 bp mRNA linear EST 05-FEB-2002
LOCUS BM469354 AGENCORT 6480665 NIH_MGC_85 Homo sapiens cDNA IMAGE:5551462
DEFINITION 5', mRNA sequence.

ACCESSION BM469354
VERSION BM469354.1 GI:18518396
KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 960)
AUTHORS NIH-MGC http://mgi.mgi.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished

COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabbs-remail.nih.gov
Tissue Procurement: Lou Staudt
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov
Plate: LLM12265 row: e column: 19
High quality sequence stop: 545.
Location/Qualifiers
1. 960
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:551482"
/tissue_type="lymphoma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC 85"
/note="Organ: lymph; Vector: PCMV-SPORT6; Site 1: NotI; Site 2: SalI; cloned unidirectionally; oligo-dT primed. Average insert size 1.867 kb. Library enriched for full-length clones and constructed by Life Technologies. Note: this is a NIH_MGC Library."

BASE COUNT 250 a 221 c 248 g 241 t
ORIGIN

Query Match 81.0%; Score 17; DB 12; Length 960;
Best Local Similarity 100.0%; Pred. No. 1.9e+03;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAAGCCCAACATGTC 17
|||||
Db 810 AAAGCCCAACATGTC 794

RESULT 15
BQ053165/c 1017 bp mRNA linear EST 29-MAR-2002
LOCUS AGENCOURT_6821899 NIH_MGC_106 Homo sapiens CDNA clone IMAGE:5934766
DEFINITION 5', mRNA sequence.
ACCESSION BQ053165
VERSION BQ053165.1 GI:19812505
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 1017)
NIH-MGC http://mgi.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished
Contact: Robert Strausberg, Ph.D.
Email: cgabbs-remail.nih.gov
Tissue Procurement: Dr. Daniel McVicar, DBS/NCI
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov
Plate: LLM2121 row: g column: 23
High quality sequence stop: 825.
Location/Qualifiers
1. 1017
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5934766"
/tissue_type="natural killer cells, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_106"

FEATURES
Source

/note="Organ: blood; Vector: pOTB7; Site_1: XhoI; Site_2: EcoRI; CDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGACGAG(G). Library constructed by Ling Hong in the Laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."

BASE COUNT 279 a 228 c 264 g 245 t 1 others
ORIGIN

Query Match 81.0%; Score 17; DB 12; Length 1017;
Best Local Similarity 100.0%; Pred. No. 2e+03;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAAGCCCAACATGTC 17
|||||
Db 1004 AAAGCCCAACATGTC 988

Search completed: February 12, 2004, 06:05:52
Job time: 1142.79 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 12, 2004, 01:54:29 ; Search time 585.854 Seconds
(without alignments)
1396.582 Million cell updates/sec

Title: US-09-692-077D-15

Perfect score: 20
Sequence: 1 ctgacgcacaacagacacac 20

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 2888711 seqs, 2045481386 residues

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GeneBml:*
1: gb_ba:*
2: gb_hcg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pac:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_scs:*
12: gb_ey:*
13: gb_un:*
14: gb_vl:*
15: em_ba:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
20: em_om:*
21: em_or:*
22: em_ov:*
23: em_pac:*
24: em_ph:*
25: em_pl:*
26: em_ro:*
27: em_scs:*
28: em_un:*
29: em_vl:*
30: em_hcg_hum:*
31: em_hcg_inv:*
32: em_hcg_other:*
33: em_hcg_mus:*
34: em_hcg_pln:*
35: em_hcg_rdd:*
36: em_hcg_mam:*
37: em_hcg_vrt:*
38: em_ey:*
39: em_hcgo_hum:*
40: em_hcgo_mus:*
41: em_hcgo_other:*

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	20	100.0	20	6	AX350503 Sequence
2	17.4	87.0	45260	8	AC134175 Drosophila
3	17.4	87.0	15455	8	AC135958 Oryza sat
4	17	85.0	17634	2	AC135242
5	16.8	84.0	1541	3	AY058358
6	16.8	84.0	71284	8	F21B23
7	16.8	84.0	91268	8	AC006837
8	16.8	84.0	91436	8	NCBI4A6
9	16.8	84.0	96232	8	ATAC010927
10	16.8	84.0	173613	3	AC007475
11	16.8	84.0	192763	3	AC007474
12	16.8	84.0	194634	2	AC020286
13	16.8	84.0	206732	2	AC109049
14	16.8	84.0	259345	2	AC102969
15	16.8	84.0	261157	2	AC103330
16	16.8	84.0	284749	2	AC113251
17	16.8	84.0	292919	3	AE003823
18	16.8	84.0	302101	1	AE016784
19	16.8	84.0	324050	1	BX251410
20	16.8	84.0	324227	1	AE016852
21	16.4	82.0	706	7	HSN332772
22	16.4	82.0	926	7	P8080COR
23	16.4	82.0	97631	2	AC141670
24	16.4	82.0	152224	2	AC141680
25	16.4	82.0	217013	2	AC106439
26	16	80.0	184862	2	AC093905
27	16	80.0	301700	1	AP005948
28	15.8	79.0	1443	1	AF351223
29	15.8	79.0	2000	6	AX656134
30	15.8	79.0	4269	8	SCYKL210W
31	15.8	79.0	4795	8	SCUBAIG
32	15.8	79.0	7799	10	AB053232S1
33	15.8	79.0	18613	8	T9B19
34	15.8	79.0	41338	2	AC017942
35	15.8	79.0	41625	3	AF022973
36	15.8	79.0	48404	8	AC079280
37	15.8	79.0	49830	6	AX059541
38	15.8	79.0	51315	9	AC134508
39	15.8	79.0	57303	2	AC020240
40	15.8	79.0	61849	3	AC004306
41	15.8	79.0	63989	8	AB013393
42	15.8	79.0	70098	8	AB025605
43	15.8	79.0	73663	8	AP002029
44	15.8	79.0	80393	8	AP000382
45	15.8	79.0	81414	8	AB024037

ALIGNMENTS

RESULT 1
AX350503
LOCUS AX350503
DEFINITION Sequence 15 from Patent WO0179561.
ACCESSION AX350503
VERSION AX350503.1 GI:18616099
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Liggett, S.B. and Small, K.M.
TITLE Alpha-2 adrenergic receptor polymorphisms
JOURNAL Patent: WO 0179561-A 15 25-OCT-2001;

Pred. No. 18 is the number of results predicted by chance to have a

FEATURES
source
Location/Qualifiers
1. .20
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"

BASE COUNT
7 a 7 c 4 g 2 t

Query Match 100.0%; Score 20; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.6;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTGATCGCCAAAGAGCAAC 20
1 CTGATCGCCAAAGAGCAAC 20

RESULT 2
AC134175 45260 bp DNA linear INV 24-SEP-2002
Drosophila pseudoobscura FOSMID DPF1-548A9 (Children's Hospital
Oakland Research Institute Drosophila pseudoobscura FOSMID Library)
complete sequence.
AC134175
AC134175.1 GI:23306009
HTG.
Drosophila pseudoobscura
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 45260)
Muzny, D. Marie, Metzker, M. Lee, Adams, C., Allen, C., Allen, H.,
Alshrooks, S., Amin, A., Anguiano, D., Anyalbechi, V., Baca, E.,
Bandaranaike, D., Biswal, K., Blair, J., Blankenburg, K., Blyth, P.,
Brown, M., Bryant, N., Buhay, C., Burch, P., Burrell, K., Calderon, E.,
Cardenas, V., Carter, K., Cavazos, I., Caesar, H., Chacko, J.,
Chavez, D., Chen, G., Chen, R., Chen, Z., Chen, J., Cleveland, C.,
Cockrell, R., Cox, C., Coyle, M., Cree, A., Davila, M. L., Davis, C.,
Davy-Carroll, L., De Anda, C., Dederich, D., Delgado, O., Denison, S.,
Deramo, C., Ding, Y., Dinh, H., Divya Khutana, Draper, H., D'Souza, L.,
Dugan-Rocha, S., Dunn, A., Durbin, K., Eaves, K., Egan, A., Escotto, M.,
Eugene, C., Falls, T., Fan, G., Fernandez, S., Finley, M., Flagg, N.,
Forbes, L., Foster, M., Foster, P., Gabisi, A., Ganta, R., Garcia, A.,
Garner, T., Garza, M., Gill, R., Grady, M., Guerra, W., Guevara, W.,
Gunaratne, P., Haaland, W., Hamilton, C., Hamilton, K., Harvey, Y.,
Havak, P., Hawes, A., Henderson, N., Hernandez, J., Hernandez, R.,
Hines, S., Hodgson, A., Hognes, M., Hollins, B., Howell, S., Hui, S.,
Hume, J., Idlebird, D., Jackson, A., Jackson, L., Jacob, L., Jiang, H.,
Johnson, B., Johnson, R., Jolivet, A., Karpathy, S., Kelly, S.,
Kelly, S., Khan, Z., King, L., Kovar, C., Kowis, C., Lebow, H., Levan, J.,
Lewis, L., Li, Z., Liu, J., Liu, J., Liu, W., Liu, Y., London, P.,
Lopez, J., Lorenzen, L., Loulseged, H., Lozano, R., Lu, X., Ma, J.,
Maheshwari, M., Mahindartine, M., Malloy, K., Mangum, A., Mangum, B.,
Mapua, P., Martin, K., Martin, R., Martinez, E., Mawhinney, S.,
McLeod, M., McNeill, T., Milosavljevic, A., Miner, G., Minig, E.,
Montenayor, J., Moore, S., Morgan, M., Morris, K., Morris, S.,
Montidesa, M., Murphy, M., Nair, L., Nankervis, C., Neal, D., Newton, N.,
Nguyen, N., Norris, S., Nwakoelamen, O., Okwunnu, G.,
Olapunnaagoon, A., Pal, S., Parks, K., Pasternak, S., Paul, H.,
Perez, A., Perez, L., Plopper, F., Polidexter, A., Popov, C.,
Primus, E., Pu, L., L., Puzos, M., Quiroz, J., Rachlin, E., Reeves, K.,
Reigh, R., Ren, Y., Reuter, M., Richards, S., Rivers, C., Rodkey, T.,
Rojas, A., Ruiz, S., Sanders, W., Savary, G., Scheer, S., Scott, G.,
Shen, H., Sibson, I., Smajs, D., Sneed, A., Sodergren, E., Song, X., Z.,
Storrelle, R., Sutton, A., Svatek, A., Tabot, P., Taylor, C., Taylor, T.,
Thomas, N., Thomas, S., Trejos, Z., Usmami, K., Valas, R., Vera, V.,
Villaana, D., Waldron, L., Walker, B., Wang, J., Wang, Q., Wang, S.,
Warren, J., Warren, R., Wei, X., White, F., Williams, G., Willson, R.,
Wiczek, R., Wooden, H., Worley, K., Wright, R., Wu, J., Yakub, S.,
Yen, J., Yoon, L., Yoon, V., Yu, F., Zhang, J., Zhou, D., Zhou, K.,
Weinstock, G. and Gibbs, R. A.

TITLE
JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

Direct Submission
Unpublished
2 (bases 1 to 45260)
Morley, K.C.
Direct Submission
Submitted (24-SEP-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
Sequencing is completed to a minimum standard of double strand
coverage with a minimum of 2 clones and 2 reads with no ambiguities
or 2 chemistries with a minimum of 2 clones and 3 reads with no
ambiguities. If the sequence quality does not meet this standard,
it will be indicated in the annotation.
Location/Qualifiers
1. .45260
/organism="Drosophila pseudoobscura"
/mol_type="genomic DNA"
/db_xref="taxon:7237"
/clone="DPF1-548A9"

BASE COUNT 11756 a 10970 c 10929 g 11605 t

Query Match 87.0%; Score 17.4; DB 3; Length 45260;
Best Local Similarity 94.7%; Pred. No. 1.4e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CTGATCGCCAAAGAGCAAC 19
1 CTGATCGCCAAAGAGCAAC 19

RESULT 3
AC135958 154555 bp DNA linear PLN 25-APR-2003
Oryza sativa chromosome 3 BAC OSJNBa0059E14 genomic sequence,
complete sequence.
AC135958
AC135958.2 GI:29837774
HTG.
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Eriarthroidea; Oryzaceae; Oryza.
1 (bases 1 to 154555)
Buell, C. R., Yuan, Q., Ouyang, S., Liu, J., Gansberger, K., Jones, K. M.,
Overton, II, L. L., Teitlin, T., Kim, M. M., Bera, J. J., Jin, S. S.,
Padresh, D. W., Tallon, L. J., Koo, H., Ziemann, V., Hsiao, J., Blunt, S.,
Vanaken, S. S., Riedmuller, S. B., Uterback, T. T., Feldlyum, T. V.,
Yang, Q. Q., Haas, B. J., Sun, B. B., Peterson, J. J., Quackenbush, J.,
White, O., Salzberg, S. L. and Fraser, C. M.
Oryza sativa chromosome 3 BAC OSJNBa0059E14 genomic sequence
Unpublished
2 (bases 1 to 154555)
Buell, R.
Direct Submission
Submitted (01-NOV-2002) The Institute for Genomic Research, 9712
Medical Center Dr, Rockville, MD 20850, USA
3 (bases 1 to 154555)
Buell, R.
Direct Submission
Submitted (15-APR-2003) The Institute for Genomic Research, 9712
Medical Center Dr, Rockville, MD 20850, USA
4 (bases 1 to 154555)
Buell, R.
Direct Submission
Submitted (25-APR-2003) The Institute for Genomic Research, 9712
Medical Center Dr, Rockville, MD 20850, USA, rbuel1@icr.org
On Apr 15, 2003 this sequence version replaced gi:24462343.
Address all correspondence to: rice@icr.org
BAC clone OSJNBa0059E14 is from Oryza sativa chromosome 3
The orientation of the sequence is from SP6 to T7 end of the BAC

This BAC overlaps with rice BAC OSJNB0015102 (AC135563).

mRNA	complement(join(<2338..2570,2665..>3123)) /gene="OSJNBa0059E1.4"
CDS	complement(join(2499..2570,2665..3123))

repeat_region

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CDS        join(4169. .4410,4495. .4975,5067. .5246)

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/note=ccontains Pfam profile PF03763 (remorin, C termina
region); EST BE041106, D41920, AU097433 from this gene"
join(9301..10065,10558..11079)
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join(9403..10065,10558..10749)
CDS

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gene /rpt family="(CCG)n"
complement(12645. .14126

mRNA	complement (<12645. .>14126 /gene="OSJNBa0059E14.4"
CDS	complement (12645. .14126)

/product="putative immediate-early salicylate-induced

repeat_region

gene 15663. .21236

mRNA

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CDS      join(16048. .16059,16193. .16379,16712. .16962,17065. .17164
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/note="consains Pfam profile PF03763 (remorin, C terminal region). EST:BD041106.D41920.AF097433 from this gene"
 join(9301..10065,10558..11079)
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 TMQPGDNGGNGDELTSGDELTETNPALVPSDPIATPSASQSLQVLPAGP
 SPAPVAPQVAKKGEVETKTSANQTLQVAKINRRFGEVYVINGETVETDYSKAMLK
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 VPTKRSFP"
 9422..9587
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 complement(12645..14126)
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 /note="similar to immediate early salicylate induced
 glucosyltransferase GB:AB36653 GI:1685005 (Nicotiana
 tabacum)"
 complement(<12645..>14126)
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 glucosyltransferase"
 /protein_id="AAP1423.1"
 /db_xref="GI:30103010"
 /translation="MAAATADGGGRRLRVFLPPFAGHLIPMTDLACLMAASTD
 AVEAEAMATVPANAAATADVAGNAVVCYPPPDVGLAGVECLGAAAHDTMRY
 RVADLRDPHSESLRHRRDIAVAQVPMWATVGAELVGRLETFNPGVPOLAMN
 NLVAVRDPHSGADGPPVPCMPGRETTPVSELPDLYODHLMSMPRTASQ
 LAGGVVNTPALAEPYCDSESRVARRAIFYGPGVSGSRAAAARVGGGDYDCL
 RMSTKSGSVVYVCESSMAVSLVTPTRELAGLEASNPFLMTVRSDSGGSGRWE
 BEGMEERMEBGGVRCMAVQALVAVTGTGATGICGNSVLEAAAGVPLMTPLV
 FEQILNRLVTEVAEFARVWEGSGGKRGVRAEATVPAQVIAARVAGFMAGGGR
 ERAAMATLAESARVAVGNSWMDIRLLQDLDAVASQP"
 13319..13354
 /rpt_family="GC-rich"
 13913..13963
 /rpt_family="CCG.n"
 15663..21236
 /gene="OSUNBA0059E14.5"
 /note="highly similar to cellulose synthase catalytic
 subunit GB:AAC39336 GI:2827143 (Arabidopsis thaliana);
 EST:AO064228.AU176398, CB096725.AA751514 from this gene"
 join(15663..16059,16193..16379,16712..16962,17065..17164
 17243..17429,17725..17991,18085..18430,18519..18656,
 18739..18864,18950..19162,19322..19577,19773..19975,
 20219..20569,20652..21236)
 /gene="OSUNBA0059E14.5"
 join(16048..16059,16193..16379,16712..16962,17065..17164
 17243..17429,17725..17991,18085..18430,18519..18656,
 18739..18864,18950..19162,19322..19577,19773..19975,
 20219..20569,20652..21236)
 /codon_start=1
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 /protein_id="AAP1426.1"
 /db_xref="GI:30103013"
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 EYKSDSQAPQCKTKRKHKSSPILGSDSDVADADASDVNTPTSGNDHKKIA
 BRMLTNGNSGRNDIYHVSZTSGELGHPYVSGELPRYISLTHSQISGILPASP
 DHMMSYVGNIGRGHPYVYHNSPNSGRSGGLGVAKVAGVDGKMKDKALPMAN
 GTSJASPEGVGDIDASTQMEDMLNDETROPISRKYVLISSSRINREYVILRL
 IGLTILPHYITNPYNAVYELMLSVICELMFWLSWIIDOPKMSPIRETYLDLAL
 RYDEGEPQLAPVDIFSVYVDPMKRPPLVYANTVSLIANDVPYDKSCYSDGGA
 NLETFDLATSEFRKAPVCKEKGWITSEPAEPYPAQKTDYLDKRVQSVFGRAMK
 MEETFDYRVAVALAAKQVPCGGWIMQCTPWPNGNTDHEGMIVELFVSGGRADTE

GNEPLRYVVSREKRGFOHKKAGAMALVRSAYL/TNGOYLTLNDCDHYNNKAL
 REMCMFLMPNLRRCVCTQFPRFPGCTIRNDRYARNRYPFDINRGIDGAGPVV
 AGCGVFNRLALVGPPIKQKRGYSSLCGKTKYSKREKSTKSKHKKVDSVP
 VFLNEDIERGIESGFDDEKSLMSQMSLEKRGSSVASTLWEGVQSATPS
 LLEKALHVISCGYEDSDWGTETIGVSTVEDILTGFOHARQMSIYCMKRPAPK
 GSAPELWSDRLNOVLFWALGSAVLEFSPHCPWYGGRLKFLERAYINTIYPLTS
 IPELLICILPALCLLTGKFLIPETISNPAISWISLPLSIPTGCIEMRWSGIDTWM
 RNEQFWVIGSISNHLFVNRQGLKQVAGIDPTTSKASDEGDAELMYMKMTLL
 IPPTLILNVGVNAGISVAINSGYOSMPLFGKLPAPWYVHLVYPLKGLMGRON
 RPTPIVVMALILASIFSLWVRIDPPTTRVGTPTQKGINC"
 complement (21685..24525)
 /gene="OSJNB0059E14.6"
 /note="similar to polygalacturonase precursor GB:AC26512
 GI:3320462 (Cucumis melo)"

Query Match 87.0%; Score 17.4; DB 8; Length 154555;
 Best Local Similarity 94.7%; Pred. No. 1.5e+02;
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 2 TGATGCCAAGCAGCAAC 20
 Db 26680 TGATGCCAAGCAGCAAC 26698

RESULT 4
 AC135242 176534 bp DNA linear HTG 28-FEB-2003
 LOCUS Oryza sativa (japonica cultivar-group) chromosome 11 clone
 OSJNB0070D14, ** SEQUENCING IN PROGRESS ***, 6 ordered pieces.
 AC135242
 AC135242.4 GI:28604237

ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 HTG: HTGS PHASE2.
 Oryza sativa (japonica cultivar-group)
 Oryza sativa (japonica cultivar-group)
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliopsida; Liliopsida; Poales; Poaceae;
 Euphorbiaceae; Oryzae; Oryza.
 1 (bases 1 to 176534)
 Swain, S.C., Sureshbabu, K., Singh, A., Pal, S., Gaikwad, K.,
 Ghazi, I.A., Dixit, A., Yadav, M., Srivastava, S., Bhargava, A.,
 Pal, A.K., Dalal, V., Batra, K., Sharma, T.R., Mohapatra, T. and
 Singh, N.K.

REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 REFERENCE
 AUTHORS
 Unpublished
 2 (bases 1 to 176534)
 Swain, S.C., Sureshbabu, K., Singh, A., Pal, S., Gaikwad, K.,
 Ghazi, I.A., Dixit, A., Yadav, M., Srivastava, S., Bhargava, A.,
 Pal, A.K., Dalal, V., Batra, K., Sharma, T.R., Mohapatra, T. and
 Singh, N.K.

TITLE
 JOURNAL
 REFERENCE
 AUTHORS
 Direct Submission
 Submitted (10-OCT-2002) IIRGS, NRC on Plant Biotechnology, Indian
 Agricultural Research Institute, LBS Centre, New Delhi, Delhi
 110012, India
 3 (bases 1 to 176534)
 Swain, S.C., Sureshbabu, K., Singh, A., Pal, S., Gaikwad, K.,
 Ghazi, I.A., Dixit, A., Yadav, M., Srivastava, S., Bhargava, A.,
 Pal, A.K., Dalal, V., Batra, K., Sharma, T.R., Mohapatra, T. and
 Singh, N.K.

TITLE
 JOURNAL
 REFERENCE
 AUTHORS
 Direct Submission
 Submitted (28-FEB-2003) IIRGS, NRC on Plant Biotechnology, Indian
 Agricultural Research Institute, LBS Centre, New Delhi, Delhi
 110012, India
 On Feb 28, 2003 this sequence version replaced GI:27502456.

COMMENT
 * NOTE: This is a 'working draft' sequence. It currently
 * consists of 6 contigs. Gaps between the contigs
 * are represented as runs of N. The order of the pieces
 * is believed to be correct as given, however the sizes
 * of the gaps between them are based on estimates that have
 * provided by the submitter.
 * This sequence will be replaced
 * by the finished sequence as soon as it is available and
 * the accession number will be preserved.
 * 1 49567: contig of 49567 bp in length

* 49568 49667: gap of unknown length
 * 49668 97492: contig of 47825 bp in length
 * 97493 97592: gap of unknown length
 * 97593 145324: contig of 47732 bp in length
 * 145325 145424: gap of unknown length
 * 145425 148804: contig of 3380 bp in length
 * 148805 148904: gap of unknown length
 * 148905 165731: contig of 16827 bp in length
 * 165732 165832: gap of unknown length
 * 165832 176534: contig of 10703 bp in length.

FEATURES
 source
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 /organism="Oryza sativa (japonica cultivar-group)"
 /mol_type="genomic DNA"
 /db_xref="taxon:39947"
 /chromosome="11"
 /clone="OSJNB0070D14"
 /note="(japonica cultivar-group)"
 BASE COUNT 50370 a 38483 c 37230 g 49875 t 576 others

Query Match 85.0%; Score 17; DB 2; Length 176534;
 Best Local Similarity 100.0%; Pred. No. 2.6e+02;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 ATGCCAAGCAGCAAC 20
 Db 80421 ATGCCAAGCAGCAAC 80437

RESULT 5
 AY058358 1541 bp mRNA linear INV 16-OCT-2001
 LOCUS Drosophila melanogaster GH12788 full length cDNA.
 ACCESSION AY058358
 VERSION AY058358.1 GI:16182835
 KEYWORDS FLI_CDNA.
 SOURCE Drosophila melanogaster (fruit fly)
 ORGANISM Drosophila melanogaster
 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 Neoptera; Endopterygota; Diptera; Brachyera; Muscomorpha;
 Euphytoidae; Drosophilidae; Drosophila.

REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 REFERENCE
 AUTHORS
 Direct Submission
 Submitted (08-OCT-2001) Berkeley Drosophila Genome Project,
 Lawrence Berkeley National Laboratory, One Cyclotron Road,
 Berkeley, CA 94720, USA
 Sequence submitted by:
 Berkeley Drosophila Genome Project
 Lawrence Berkeley National Laboratory
 Berkeley, CA 94720

COMMENT

This clone was sequenced as part of a high-throughput process to
 sequence clones from Drosophila Gene Collection 1 (Rubin et al.,
 Science 2000). The sequence has been subjected to integrity checks
 for sequence accuracy, presence of a polyA tail and continuity
 within 100 kb in the genome. Thus we believe the sequence to
 reflect accurately this particular cDNA clone. However, there are
 artifacts associated with the generation of cDNA clones that may
 have not been detected in our initial analyses such as internal
 priming, priming from contaminating genomic DNA, retained introns
 due to reverse transcription of unspliced precursor RNAs, and
 reverse transcriptase errors that result in single base changes.
 For further information about this sequence, including its location
 and relationship to other sequences, please visit our web site
 (http://fruitfly.berkeley.edu) or send email to
 cdna@fruitfly.berkeley.edu.
 Location/Qualifiers
 1..1541

/organism="Drosophila melanogaster"
/mol_type="mRNA"
/strain="Y; cn bw sp"
/db_xref="taxon:7227"
/map="48B2-48E2"
1..1541
/gene="CG17509"
/note="alignment with genomic scaffold AE003823"
/db_xref="FLYBASE:FBgn0033676"
28..1275
/gene="CG17509"
/note="Longest ORF"
/codon_start=1
/product="GH12788p"
/protein_id="AAL13587.1"
/db_xref="GI:16182836"
/db_xref="FLYBASE:FBgn0033676"

CDS

BASE COUNT 435 a 376 c 390 g 340 t
ORIGIN
Query Match 84.0%; Score 16.8; DB 3; Length 1541;
Best Local Similarity 90.0%; Pred. No. 2.5e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
1 CTGATGCCCAACGACGAC 20
Db 787 CTGATGCCCAACGACGAC 806

RESULT 6
LOCUS F21B23 71284 bp DNA linear PLN 27-JUL-2000
DEFINITION Arabidopsis thaliana BAC F21B23.
ACCESSION AF262038
VERSION AF262038.1 GI:9502148
KEYWORDS
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Rosidae; eudicotyledons; core eudicots;
1 (bases 1 to 71284)
2 (bases 1 to 71284)
The A. thaliana Genome Sequencing Project.
REFERENCE
AUTHORS Washington University Genome Sequencing Center.
TITLE The A. thaliana Genome Sequencing Project.
JOURNAL Unpublished
AUTHORS Wilson R.
TITLE Direct Substitution
JOURNAL Submitted (01-MAY-2000) Department of Genetics, Washington
UNIVERSITY, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
COMMENT
Submitted by:
Genome Sequencing Center
Department of Genetics, Washington University,
St. Louis, MO 63108, USA
e-mail: r.wilson@wustl.edu

NOTICE: This sequence may not be the entire insert of this clone.
It may be shorter because we only sequence overlapping sections
once, or longer because we provide a small overlap between

neighboring submissions.

This sequence was finished as follows unless otherwise noted:
all regions were double stranded, sequenced with an alternate
chemistry or covered by high quality data (i.e., phred quality
>= 30); an attempt was made to resolve all sequencing problems,
such as compressions and repeats; all regions were covered by
sequence from more than one m3 subclone.

NOTES:

Coding sequences below are predicted from computer analysis, using
the program GeneFinder (P. Green and L. Hillier, ms in preparation).

FEATURES

source

1..71284
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/mol_type="genomic DNA"
/cultivar="Columbia"
/db_xref="taxon:3702"
/chromosome="v"
/map="unknown"
/clone="F21B23"
/gene="F21B23.3"
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4709..4932,5136..5331,5530..5597,5670..5844,5931..5978,
6028..6081,6258..6437,5567..6679,6803..6985,7177..7234,
7456..7515,7615..7656,7752..7879,7977..8112,8243..8278,
8454..8570,8662..8724,8808..8909)
/note="contains similarity to Drosophila melanogaster
bcdNA.GH03694 (GB:AA055412); coded for by A. thaliana cDNA
H36877; coded for by A. thaliana cDNA N96846; coded for by
A. thaliana cDNA AA651310"
/codon_start=1
/protein_id="AAF88009.1"
/db_xref="GI:9502156"
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FGGAFSGSHPSDNDRLSLYLTNGVAGVAFPLASDDFTSTPAIVOLELGRS
KLLFVANSQGLVVCVSVNKKLYTESIAEKVGADGACVASEQOILAVGTRGM
VELYDLSHISILRTVSLHDGWSADYTPVANNIANTPNSAFVAGMSKRLAVGASVS
GRLMSYVROILGTSTSPKINPKODCKEPTMSGSAIOMDEYGRLEPATEASDR
ILAFRGKCCINRGVSGKTVYRVGVISQMPVOHVAASEDKYLAIVGLHLLIYDI
RKKRVVRGDSVQEQIHCCKLMIGKIVTCNTYBASTYELLPRTPLHDOSSILC
RKVLGKPMVNVQDYILVSLPFIHVHYVHYVIGELTPSSKADQLHREGLDND
LSSDLSDRPSRCLIRNGELSLDLVGRERBLTDSVLEFWVTCGSEBKTNLVEE
VSLMDYGRMGCGCPAPKCLVTYLVLPVPSLADDPMDQDFQLDELFEDEYV
PLGLPNGVVVGVGORMSPSASAFACEPPTROTILHLLRHLORXKEBALLL
AOLSAKHFHSCLEMLFTVPDAISRPENRNOISGRGHKXKLSLAKADLIKKF
BEYIVVAVNARKTDARHWADLPSAAGSITLFEDCFQKRYRTACIYLVIAKLEGV
AVSOYCALRLQATLDESILYDLAGELVRLASGRDIBQAPTESDLSKGLFLIFG
SSHKSSLDKSSPFKEQSPHVASVKSILSHSAYMSGELSKLVAFVGQTFDLYNF
AAGLEIGOKLQMSLEIQRDLDAEFLAQCYSVFKEWIVLVTLTLORESVLDIFRYD
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/gene="F21B23.5"
complement(join(10977..11226,11408..11588,11647..11830))
/gene="F21B23.5"
/note="contains similarity to aminocyclopropanecarboxylate
synthases"
/codon_start=1
/evidence=not experimental
/protein_id="AAF88004.1"
/db_xref="GI:9502151"
/translation="MSQGCENQSLKSLASDKHGSAPYFPGMKAYDNNPPPTNP
OGVIMGLAENOVRLIYFVYICQLSDILKEMIKENPHASICTAEDIDFSDIAY
PDYVGLNKFROVPIFSLRTICIQIMCCTENKQALATMEBARAGRVAFERV
VMSGATGANETIMFCLADPGDAFLPPTTYAIVYIHTLVFK"
complement(14503..16686)
/gene="F21B23.6"
complement(14503..16686)

CDS

gene

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/gene="F21B23.6"
/notes="similar to a large family of Arabidopsis thaliana
salt inducible protein-like proteins; contains similarity
to Pfam family PF01535 (Domain of unknown function),
score=340.5, E=1.9e-98, N=2"
/codon_start=1
/evidence=not experimental
/protein_id="AAF8005.1"
/db_xref="GI:9502152"
/translation="MSIMLSISRRQNSYLLNHSRPLRRPVDVDPREPKESQEFV
VVFVKTLQNTPDHMASSSLALVSSSSASPLVFSQITRRLSYSLSAIFEFYLD
AKSOSIKRRSESLALQSYIFAGSEPPDRLRLYLIAEKNIPLVITATKLIR
WFRMGVNNQSVLYERLDNMKNQSVNNVVVLLRNGLVDAFKYIDSLCKANAN
PAPRTADVLHEVWKERLITEKKIILSRFSHVSNSVWLTRFKISLCKANAN
TAMDIISDLMKKTPIEAPFNALLSLGRNMISPMNDLVLMDEPKLRPVYITGI
LINTCKSRVDLALVFEQMRGRITDDGVTKADSIHRTLLDLCYGRKLKEABL
LVYMKLEERCVPNAVYVNCIDYCRAGSKLETKAEVSRKKEDEIKPVNTVNTVIGG
MCRHGHGLNMAVVFPMMEKEGKGNVTVVTLTHACSVSNVEMKAMVEMKLEACS
PDAKITVYALISGLQVRRDHAIRVYKLEGGFSLDLAANNLIGLPCDKNAEYV
EMLTDMKEGKGPDSITVNTLISFGKHQFESVEMMEQREDGLDPTVYTGAVTD
AYCSVGHIDPAIKLFPDMGLSKVNPVTVYNTLINAESKLGNGOALSKEEMKMKM
VRNVEYTNALFKLNEKGTGRTLKMDMEVHLVQIRSORP"
/complement (24152..26942)
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/complement (join(24152..24287,24374..24440,24665..24872,
25152..25208,25625..25735,26021..26062,26667..26942))
/gene="F21B23.7"
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recognition motif, (a.k.a. RRM, RBD, or RNP domain)),
score=42.1, E=1.3e-08, N=1"
/codon_start=1
/evidence=not experimental
/protein_id="AAF8006.1"
/db_xref="GI:9502153"
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NPITFYVLDVGNVAKVDEDEVLSRGLDLEVLSSRLQVLEDMQKFKLLGL
GROKIMEKEGPGKGYFVTFRCDDAAAILNNLTVREQNGRNGRNFIFRY
NHYALYIKNLPDITQERLKLFEHNGKILKVIIPAKGKEDSRGFVAVERTSV
MRLKNTREYRIGDHAAGSMMPIMLPDRIRIVYIQQLAAMPQPPRPSPYRGG
SGSSSSKQSSDNGRGRNYPY"
/complement (27206..29561)
/gene="F21B23.8"
/complement (join(27206..27759,28027..28122,28481..29561))
/gene="F21B23.8"
/notes="contains similarity to Drosophila
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heparan sulfate-N-deacetylase/N-sulfotransferases"
/codon_start=1
/evidence=not experimental
/protein_id="AAF8007.1"
/db_xref="GI:9502154"
/translation="MENGVEYTHKDTSLKPVSSSSSSSEEFPRFVSIIIMRLD
LIPKLAIGRALLFGYIGMLTKTVLYRRKSNRECEKLEKEMRRKMRKMERLRLD
KGTVEVLHKEGLEKPLMSFEKPTDRNEMLSSISKVGSEKLELVNSHVEDLPDK
IHETKVARARAREIAGIEINKEKRDVNTGSDSDISIQSKSLPHGLTHSVGD
DDKDERLGTSDSENTELSAFAVPMLANGANGVDSGAPKKVSNVPLVPD
GVIQASVYTKQLSMKNKSTGRKSRVRSVYEAKEFLRSGEELRQESLOMAQSD
EITFPQSDDERGVARKKIKVNDKNIILVYSEVNDLEMMKDEKLRIVCVNDNEA
DGVSVDPLEKIIIPMKGPSIDKPEPLNTHREBLFSGKASVSPVYCEGSSMO
ELSSASSENTLTPSSSETTSQPKIVVSGDSVRRPGKSGKWTQTKMSRGFELM
YNAETIDPEKAVMRMDGMDLDRITTEDEIDDAIDIMEKLPERNKKKEKLNKLKREM
ELFQPOAVNS"
/gene="F21B23.2"
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40816..40861,40959..41072,41156..41317,41364..41443)
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family), score=29.7, E=4e-06, N=2"
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/evidence=not experimental
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/db_xref="GI:9502150"

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Query Match      84.0% Score 16.8; DB 8; Length 71284;
Best Local Similarity 90.0%; Pred. No. 3.3e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 CTGATGCCCAACGAGCAAC 20
DB      18720 CTGATGCCCAATGAGCAAC 18739

RESULT 7
AC006837/c
LOCUS
DEFINITION
Arabidopsis thaliana chromosome 2 BAC F23H14 genomic sequence,
complete sequence.
ACCESSION
AC006837
VERSION
AC006837.16 GI:20197903
KEYWORDS
HTG.
SOURCE
Arabidopsis thaliana (thale cress)
ORGANISM
Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsids.
1 (bases 1 to 91268)
Town,C.D., Haas,B.J., Wu,D., Maiti,R., Hannick,L.I., Chan,A.P.,
Tallon,L.J., Rooney,T., Utterback,T.R., Vannick,S.E.,
Feldblyum,T.V., White,O. and Fraser,C.M.
Arabidopsis thaliana chromosome 2 BAC F23H14 genomic sequence
Unpublished
2 (bases 1 to 91268)
Lin.X.
Direct Submission
Submitted (09-MAR-2000) The Institute for Genomic Research, 9712
Medical Center Dr., Rockville, MD 20850, USA
3 (bases 1 to 91268)
Town,C.D. and Kaul,S.
Direct Submission
Submitted (27-FEB-2002) The Institute for Genomic Research, 9712
Medical Center Dr., Rockville, MD 20850, USA, cdtowm@tigr.org
On Apr 18, 2002 this sequence version replaced gi:5598619.
Address all correspondence to: atot@tigr.org

COMMENT
BAC clone F23H14 is from Arabidopsis thaliana chromosome 2
clone.
The orientation of the sequence is from SP6 to T7 end of the BAC
clone.
Genes were identified by a combination of several methods: Gene
prediction programs including Genescan* (Chris Burge,
http://CCR-081.mit.edu/GENSCAN.html), GEMMA* (Mark Borodovsky,
http://genemark.biology.gatech.edu/Gememark/), Glimmer* (a variant
of Glimmer), see Michaela Perlea,
http://www.tigr.org/softlab/glimmer.htm/glimmerm.html, and
GeneSplicer (Michaela Perlea and Steven Salzberg,
http://www.tigr.org), searches of the complete sequence against a

```


peptide database and the plant EST database at TIGR (<http://www.tigr.org/tdb/cgi.shtml>). Annotated genes are named to indicate the level of evidence for their annotation. Genes with similarity to other proteins are named after the database hits. Genes without significant peptide similarity but with EST similarity are named as unknown proteins. Genes without protein or EST similarity, that are predicted by more than two gene prediction programs over most of their length are annotated as hypothetical proteins. Genes encoding rRNAs are predicted by tRNAscan-SE (Sean Eddy, <http://genome.wustl.edu/eddy/tRNAscan-SE/>). Simple repeats are identified by RepeatMasker (Arin Smit, <http://ftp.genome.washington.edu/RM/RepeatMasker.html>).

FEATURES

```
source
1..91268
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/cultivar="Columbia"
/db_xref="taxon:3702"
/chromosome="2"
/map="ml398"
/clone="F23H14"
1..9372
/notes="rDNA 10.5 kbp repeat unit"
1..88
/rpt_family="Rf:rDNA repeat of 18S rDNA, intergenic
spacer, 5.8S rDNA, spacer, 25S rDNA, spacer entire repeat
unit is 10.5 kbp, 2 loci of ~3.5 Mbp on chromosomes II and
IV, 670 copies#Rf:ATR0026|X52322|X15550 10.5 kbp rDNA
repeat"
1..85
/rpt_family="Rf:Spacer between 25S and 18S rDNAs part of
the 10.5 kbp rDNA repeat#Rf:ATR0032|X15550 intergenic
spacer between 25S and 18S rDNAs"
80..2705
/rpt_family="Rf:Spacer between 25S and 18S rDNAs part of
the 10.5 kbp rDNA repeat#Rf:ATR0032|X15550 intergenic
spacer between 25S and 18S rDNAs"
85..2705
/rpt_family="Rf:rDNA repeat of 18S rDNA, intergenic
spacer, 5.8S rDNA, spacer, 25S rDNA, spacer entire repeat
unit is 10.5 kbp, 2 loci of ~3.5 Mbp on chromosomes II and
IV, 670 copies#Rf:ATR0026|X52322|X15550 10.5 kbp rDNA
repeat"
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the 10.5 kbp rDNA repeat#Rf:ATR0032|X15550 intergenic
spacer between 25S and 18S rDNAs"
414..503
/rpt_family="Rf:rDNA repeat of 18S rDNA, intergenic
spacer, 5.8S rDNA, spacer, 25S rDNA, spacer entire repeat
unit is 10.5 kbp, 2 loci of ~3.5 Mbp on chromosomes II and
IV, 670 copies#Rf:ATR0026|X52322|X15550 10.5 kbp rDNA
repeat"
414..501
/rpt_family="Rf:rDNA repeat of 18S rDNA, intergenic
spacer, 5.8S rDNA, spacer, 25S rDNA, spacer entire repeat
unit is 10.5 kbp, 2 loci of ~3.5 Mbp on chromosomes II and
IV, 670 copies#Rf:ATR0026|X52322|X15550 10.5 kbp rDNA
repeat"
447..500
/rpt_family="Rf:rDNA repeat of 18S rDNA, intergenic
spacer, 5.8S rDNA, spacer, 25S rDNA, spacer entire repeat
unit is 10.5 kbp, 2 loci of ~3.5 Mbp on chromosomes II and
IV, 670 copies#Rf:ATR0026|X52322|X15550 10.5 kbp rDNA
repeat"
449..502
/rpt_family="Rf:Spacer between 25S and 18S rDNAs part of
the 10.5 kbp rDNA repeat#Rf:ATR0032|X15550 intergenic
spacer between 25S and 18S rDNAs"
1459..1829
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spacer, 5.8S rDNA, spacer, 25S rDNA, spacer entire repeat
unit is 10.5 kbp, 2 loci of ~3.5 Mbp on chromosomes II and
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IV, 670 copies#Rf:ATR0026|X52322|X15550 10.5 kbp rDNA
repeat"
1459..1519
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the 10.5 kbp rDNA repeat#Rf:ATR0032|X15550 intergenic
spacer between 25S and 18S rDNAs"
1461..1829
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the 10.5 kbp rDNA repeat#Rf:ATR0032|X15550 intergenic
spacer between 25S and 18S rDNAs"
1461..1519
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spacer, 5.8S rDNA, spacer, 25S rDNA, spacer entire repeat
unit is 10.5 kbp, 2 loci of ~3.5 Mbp on chromosomes II and
IV, 670 copies#Rf:ATR0026|X52322|X15550 10.5 kbp rDNA
repeat"
1769..2139
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the 10.5 kbp rDNA repeat#Rf:ATR0032|X15550 intergenic
spacer between 25S and 18S rDNAs"
1771..2139
/rpt_family="Rf:rDNA repeat of 18S rDNA, intergenic
spacer, 5.8S rDNA, spacer, 25S rDNA, spacer entire repeat
unit is 10.5 kbp, 2 loci of ~3.5 Mbp on chromosomes II and
IV, 670 copies#Rf:ATR0026|X52322|X15550 10.5 kbp rDNA
repeat"
2079..2139
/rpt_family="Rf:Spacer between 25S and 18S rDNAs part of
the 10.5 kbp rDNA repeat#Rf:ATR0032|X15550 intergenic
spacer between 25S and 18S rDNAs"
2081..2139
/rpt_family="Rf:rDNA repeat of 18S rDNA, intergenic
spacer, 5.8S rDNA, spacer, 25S rDNA, spacer entire repeat
unit is 10.5 kbp, 2 loci of ~3.5 Mbp on chromosomes II and
IV, 670 copies#Rf:ATR0026|X52322|X15550 10.5 kbp rDNA
repeat"
2706..9364
/rpt_family="Rf:rDNA repeat of 18S rDNA, intergenic
spacer, 5.8S rDNA, spacer, 25S rDNA, spacer entire repeat
unit is 10.5 kbp, 2 loci of ~3.5 Mbp on chromosomes II and
IV, 670 copies#Rf:ATR0026|X52322|X15550 10.5 kbp rDNA
repeat"
2706..4513
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2706..4513
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2706..4513
/product="18S rRNA"
2706..4513
/rpt_family="Rf:18S rDNA contained within the 10.5 kbp rDNA
repeat#Rf:ATR0027|X16077 18 S rDNA"
4514..4781
/rpt_family="Rf:Spacer between 18S and 5.8S rDNAs part of
the 10.5 kbp rDNA repeat#Rf:ATR0028|X52320|X52322|U43224
intergenic spacer between 18S and 5.8S rDNAs"
4782..4945
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4782..4945
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4782..4945
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4782..4945
/rpt_family="Rf:5.8S rDNA contained within the 10.5 kbp rDNA
repeat#Rf:ATR0029|X52320|U43225 5.8S rDNA"
4946..5133
/rpt_family="Rf:Spacer between 5.8S and 25S rDNAs part of
the 10.5 kbp rDNA repeat#Rf:ATR0030|X52320|X52322|U43225
intergenic spacer between 5.8S and 25S rDNAs"
5134..8520
/rpt_family="Rf:25S rDNA contained within the 10.5 kbp
rDNA repeat#Rf:ATR0031|X52320|X52322 25S rDNA"
8521..9364
/rpt_family="Rf:Spacer between 25S and 18S rDNAs part of
the 10.5 kbp rDNA repeat#Rf:ATR0032|X15550 intergenic
spacer between 25S and 18S rDNAs"
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repeat_region	8750..8829	/rpt family="rf:rdna repeat of 18S rDNA, intergenic spacer, 5.8S rDNA, spacer, 25S rDNA, spacer entire repeat unit is 10.5 kbp, 2 loci of ~3.5 Mbp on chromosomes II and IV, 670 copies#RF:ATR0026 X52322 X15550 10.5 kbp rDNA repeat"
repeat_region	9195..9372	/rpt family="rf:rdna repeat of 18S rDNA, intergenic spacer, 5.8S rDNA, spacer, 25S rDNA, spacer entire repeat unit is 10.5 kbp, 2 loci of ~3.5 Mbp on chromosomes II and IV, 670 copies#RF:ATR0026 X52322 X15550 10.5 kbp rDNA repeat"
repeat_region	9197..9374	
Query Match	84.0%; Score 16.8; DB 8; Length 91268;	
Best Local Similarity	90.0%; Pred. No.3.3e+02;	
Matches	18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;	
Db	53759	CTGATCGCCAAAGAGCAAC 53740
QY	1	CTGATCGCCAAAGAGCAAC 20
LOCUS	NCBI14A6	91436 bp DNA linear PLN 18-JAN-2002
DEFINITION	Neurospora crassa DNA linkage group V BAC contig B14A6.	
ACCESSION	AL670007	
VERSION	AL670007.1	GI:18376186
KEYWORDS	Neurospora crassa	
SOURCE	Neurospora crassa	
ORGANISM	Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.	
REFERENCE	1	Schulte, U., Aign, V., Hohelsel, J., Brandt, P., Partmann, B., Holland, R., Nyakatura, G., Mewes, H.W. and Mannhaupt, G. Unpublished 2 (bases 1 to 91436)
AUTHORS	German Neurospora genome project.	
JOURNAL	Direct Submission	
REFERENCE	Submitted (18-JAN-2002) MIPS, Institut fuer Bioinformatik, GSF-Forschungszentrum fuer Umwelt und Gesundheit, GmbH, Ingolstaedter Landstrasse 1, D-85764 Neuherberg, FRG, E-mail: G.Mannhaupt@gsf.de, Project Coordinator: Ulrich Schulte, Institute of Biochemistry, Heinrich-Heine-University, D-40225 Duesseldorf, E-mail: ulrich-schulte@uni-duesseldorf.de	
COMMENT	This contig is an assembly of BAC 14A6 from 1 to: 11263, and BAC 12H14 from 11264 to: 91436rev (strain OR14A); BAC clones are available at the Fungal Genetic Stock Center http://www.fgsc.net Sequencing was performed by MWG Biotech AG, Ebersberg, Germany, http://www.mwgdna.com	
FEATURES	Information on performance of analysis and a more detailed annotation of this entry and other sequences of linkage groups II and V can be viewed at: http://mips.gsf.de/proj/neurospora.	
source	location/Qualifiers	
	1..91436	/organism="Neurospora crassa"
		/mol_type="genomic DNA"
		/db_xref="taxon:5141"
		/chromosome="2"
misc_feature	1..7884	/note="overlapp to BAC B108 contig, please refer to this entry for analysis and annotation"
trna	5365..5451	/product="tRNA-Gln"
		/note="tRNA predict as a tRNA- Gln : anticodon ttg"
gene	5919..7803	/gene="B14A6.010"
gene		complement(join(5919..6185,6494..7692,7761..7803))
gene		/gene="B14A6.010"
CDS		complement(join(5919..6185,6494..7692,7761..7803))
		/gene="B14A6.010"

/note="match of 76 ESTs
contains ATP/GTP-binding site motif A (P-loop)
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contains EST gbl:AW717407, AW708782"
/codon_start=1
/product="putative protein"
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STRKSPPLLETDNVKKPKKPAPLDENKIATTDAVKKPKPTSTPEKKARVH
SSYTRRVSVSSSTKKKSTSGHTHAFTSTTKSHSRPHNLEESKGESTSHPER
HHHHHHNPNGSIIRHGCAARSSISIKPLAPAKAFAPDLAEGNPKNRPMTMHI
KRAVRKSEANRPSKPTVEBPETALPKYHPTPTAOAKTAADVAETRAKVAAA
QEBAQMDQQDQQDDQDTQPKRKKEKYAPEAMIPISRVGVNGKTAGALDITTCGA
KGAVDTGTAEAGLGGGAGVGTGAAGAAGVGTGLAAPAGLGKVTGEATGGIARAG
LGAVGTGBEGLGVTGGVGKGLDVTGGVGTGGIADVTGGVGLGGVAGTLGRGVGAATG
ITGGLGGVGVKIGGGDILGGVDVGGVNTTGGVLGLGVTLGGCGGGGQR"

exon
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complement(6494..7692)
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/number=2
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complement(7761..7803)
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10983..12122
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10983..12122
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/codon_start=1
/product="hypothetical protein"
/protein_id="CAD21304.1"
/db_xref="GI:18376188"
/translation="MSNRNPNSHLIDVNSFGSDDOCKVOEARNHSTSNAPTNHAV
IPACRRATPDSPTSVALAILDMKRKAQTPTSNITSATEPVLVTRSPNSGRPMDS
VDGLEPTFAEKRAVFISWRPKGDINPNKSSLSGLAADNCALPLTNIIPAGTIKVI
LDAGIHAFPRGVATAIAPTDRGYKSAACAKTIMFCREBAVNFQETITNKILGR
TIAVVNNRSCFQTDLPHSASRVLEICGLEIVDDIRLSRFPGANIKEPTQDVTVR
EDKRIILRWTFCSFOAOAVARKALAEWPGHIRWGIDIPMAVSVMVPTAMSLP
LPQORARVATSEVSHTPAGDLLSFSDVEGLDSKEKSDIVDF"
10983..12122
/gene="B14A6.020"
/number=1
13287..13358
/product="tRNA-Thr"
/note="tRNA predict as a tRNA- Thr : anticodon agc"
13804..15397
/gene="B14A6.030"
complement(join(13804..15031,15093..15397))
/gene="B14A6.030"
complement(join(13804..15031,15093..15397))
/note="Strong similarity to benzoate 4-monoxygenase (EC
1.14.13.12), Aspergillus niger, PIR.S12015
contains cytochrome P450 cysteine heme-iron ligand
signature [FSHPKSCVG]"
/codon_start=1
/product="probable benzoate 4-monoxygenase cytochrome
P450"
/protein_id="CAD21305.1"
/db_xref="GI:18376189"
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PCTDALMVSCRGKNRYQVDELHKRUGPVVRIDPNVVISLCDDALITITIGHNGFLN
DYDAFVDIRGELPTRDRABETRKRKIVSHTFSAKSVOQEPYMHNSLELFVQWOS
MKSKNDKAHLDCLEMFNLYLAFDVIGDLSFQGPQMGSAGADMAISSPDPAEI
YAPALEILNRGEVASATLGIPHALPKPFAYLPDPFFTKGLAVENTLAGIALACVKSRL

DNPVTRKOLLQRLMEGRDEKGEPIGREELTAELTOLIAQSDTTSSCALLPHAV
 RTPGVWQKLAELDANIPEVADVPTIDWKELEPYEAIVNEVLRPHSTGIGIPRIIP
 HPSAGQVHIGVYLPGVLSVYTESIHHSKEIWGEDEPKPERMERSTAGIKOKNAFI
 PSHGPRSCVGNNAVEMEMKLIIVATARARYEYKLLQDVMDTREGFLARKLGLKVGKTL
 RK"

complement(13804, .15031)
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 /gene="B14A6.040"
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 complement(17314, .19917)
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 /note="similarity to glucan 1, 4-alpha-glucosidase (EC
 3.2.1.3), YIR019C, Saccharomyces cerevisiae, PIR:S48478"
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 /db_xref="GI:18376190"
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 TLAASSNPFLAPVLRQSPDMAEHSHTNDNTLPRLVINLPOSIAEEEDVDVKGK
 LSELNPMADDEKDKADKACEEBOSEPMAKAEVAVQVPLAISVGSVNSLPT
 RSTPSGDHDHDERODSPITSIDDSHARPLARKSSSIYOKPVEBFDKIAVMSQ
 GEPVIRRAASKSLGPHHVDSEADFCDFEDQVKEPSPQTPPESTPEVOKPS
 SOHSGSPITSQMSWSOLGHMNELAKGALNFDLISNDKMFETSNMPLPYA
 DVSDDHITTSFNSISERKAWYIISRGSSRKINAGDDENRYVAMPTSTVCCETLQV
 RRMWEDSTAGVSLGSGISKTQKNFWDSSAEPYTLAIFGKAVPRPSSVQPLQ
 PSAPFLVDHSPAGSTAVNSLMOQHPRLQLPATTSWSSDFASAGKPLTASL
 PLTSPQAPGPKPTMDLGMSSISATLAENDDDMGEMVSPSTKATVGGFPDN
 SVSTLTSTRNGPCTTAAVMSOSDHPVSLITLSLENNNTTVPVTSAADPMASAD
 RSEFELPSQOOIGPTKSSVTPRPSMINTSPAPTPSGSTHSFDLPRTTPTTISASS
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 GGLPDLSTYMLR"
 complement(17314, .19917)
 /gene="B14A6.040"
 /number=1
 20612, .21612
 /gene="B14A6.050"
 join(20612, .20644, 20731, .21612)
 /gene="B14A6.050"
 /note="similarity to putative nucleotide binding protein,
 Homo sapiens, TREMBL:AF118394_1
 Contains ATP/GTP-binding site motif A (P-loop) [KGGVGS]"
 /codon_start=1
 /product="related to putative nucleotide binding protein
 (NUPB)"
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 /db_xref="GI:18376191"
 /translation="MSLAKVKAIVLVLSKGGVGSSTVTQALSLISLAGHVGVLVD
 DLTGSPFPMFGEIDAKTVQAGWLPITVHEADPAGVGSIRVMSLGLLRKGDV
 WVRGPKTAMVQPLSDVDFWDEDTLLIDTPGTSDEHISLAENLQKRPOLGAV
 VTTPOAVATADVRKEINFCIKNIIVLGVENMGCGVCPNGSECTINIMSGAGEVMA
 NQGVRFGRVPIIDPQFLVLTGKRPPTYAGTTVDGKDISIPAGASTSEEEVDGS
 BLVHKYKDSLAPISFKITADVIASVQ"

20612, .20644
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 20645, .20730
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 20731, .21612
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 /number=2
 23875, .25386
 gene

CDS

/gene="B14A6.060"
 23875, .25386
 /gene="B14A6.060"
 /note="identical to TREMBL:AF151380.1
 contains fumarate lyase signature [GSAVMYGNK]"
 /codon_start=1

Query Match 84.0%; Score 16.8; DB 8; Length 91436;
 Best local Similarity 90.0%; Pred. No. 3.3e+02;
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CTGATGCCCAACGAGCAAC 20
 Db 44965 CTGATGCCCAACGAGCAAC 44946

RESULT 9

ATAC010927/c ATAC010927 96232 bp DNA linear PLN 30-OCT-2002

LOCUS Arabidopsis thaliana chromosome III BAC T22K18 genomic sequence,
 DEFINITION complete sequence.

ACCESSION AC010927 GI:12408726

VERSION AC010927.5 GI:12408726

KEYWORDS HTG.
 SOURCE Arabidopsis thaliana (thale cress)

ORGANISM

Arabidopsis thaliana
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

REFERENCE 1 (bases 1 to 96232)
 Lin, X., Kaul, S., Town, C.D., Beilto, M.-I., Creasy, T.H., Haas, B.,
 Rongling, C.M., Koo, H., Fujii, C.Y., Utterback, T.R., Barnstead, M.E.,
 Bowman, C.L., White, O., Nierman, W.C. and Frazer, C.M.
 Arabidopsis thaliana chromosome III BAC T22K18 genomic sequence
 Unpublished

AUTHORS

JOURNAL 2 (bases 1 to 96232)
 Lin, X. and Kaul, S.
 REFERENCE Direct Submission
 Submitted (28-SEP-1999) The Institute for Genomic Research, 9712
 Medical Center Dr, Rockville, MD 20850, USA, xlin@igr.org
 3 (bases 1 to 96232)
 Lin, X.

JOURNAL Direct Submission
 Submitted (24-JAN-2001) The Institute for Genomic Research, 9712
 Medical Center Dr., Rockville, MD 20850, USA
 On Jan 24, 2001 this sequence version replaced gi:12280869.
 Address all correspondence to:
 Xiaoying Lin

JOURNAL The Institute for Genomic Research
 9712 Medical Center Dr.
 Rockville, MD 20850, USA
 e-mail: xlin@igr.org
 BAC clone T22K18 is from Arabidopsis chromosome III and is near the
 molecular marker C1C5D8.
 The orientation of the sequence is from SP6 to T7 end of the BAC
 clone.

REFERENCE Genes were identified by a combination of three methods: Gene
 prediction programs including GRLU (available by anonymous ftp
 from athur.epm.ornl.gov), GeneFinder (Phil Green, University of
 Washington), Gscan (Chris Burge,
 http://genomic.stanford.edu/~chris/GENSCANW.html), and NecPlantGene
 (http://www.cbs.dtu.dk/netgene/cbsnetgene.html), searches of the
 complete sequence against a peptide database and the Arabidopsis
 EST database at TIGR (http://www.tigr.org/tdb/at.html).
 Annotated genes are named to indicate the level of evidence for
 their annotation. Genes with similarity to other proteins are named
 after the database hits. Genes without significant peptide
 similarity but with EST similarity are named as 'unknown' proteins.
 Genes without protein or EST similarity, that are predicted by more
 than two gene prediction programs over most of their length are
 annotated as 'hypothetical' proteins. Genes encoding tRNAs are
 predicted by tRNAscan-SE (Sean Eddy,
 http://genome.wustl.edu/eddy/tRNAscan-SE/). Simple repeats are

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identified by repeatmasker (Arjan Smit,
<http://ftp.genome.washington.edu/RM/RepeatMasker.html>). Regions of
 genomic sequence that are not annotated as genes but have predicted
 exons by GRail are annotated as misc features.

FEATURES

source

1..96232
 Location/Qualifiers

/organism="Arabidopsis thaliana"

/mol_type="genomic DNA"

/cultivar="Columbia"

/db_xref="taxon:3702"

/chromosome="III"

/map="C1C5D8"

/clone="T22K18"

1..708

/note="overlap with BAC clone F14P13
 (AC009400:87230..87937)."

/complement (48..91)

/note="exon predicted by xgrail, quality marginal"

/complement (437..495)

/note="exon predicted by xgrail, quality good_shadowexon"

<877..>3349

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/note="similar to folylpolyglutamate synthetase
 GB:AA87568 (Homo sapiens)"

join(<877..929,1009..1069,1403..1486,1588..1644,
 1737..1797,1880..1926,2058..2148,2480..2619,2713..2955,
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 3312..3467,3548..3744,3890..3949)

/gene="T22K18.1"

/codon_start=1

/product="putative folylpolyglutamate synthetase"

/protein_id="AA04408.1"

/db_xref="GI:6143861"

/translation="MTSPHLIDYRFRRIDGLDISEKEFLQYFWECKLAKKAVDG
 LTMPLPFLAFKIFVCEKVDVAIEVGLGKLDSTNVIQKPVCGASGDMH
 DILGNTADIAFLHAKGFKPOIPAFVTPOLSEMDVIOKTANNLEVTIVLPEPKLD
 GVTIGLSGDQLVNAVLAVLSRCWLORTGKWKIKPFNEKEITIPAFRGLATARL
 HGRAQVADVDSQDSSDSEMTFCGLITFYLDGASPESEMGCRWFSSAVGADSL
 STAILPNCMEVRDPQVLPRLVYTCASSGTHSRALFVSMSTYKNGVIGASAIQSD
 TRKDLTQFRLQRLMEKSIQGDAGIDHTLCKEITALPDPFLCGDAQCQGPAGT
 PVSSAWMPSPLPTINMLRDCVRNPSELKLEVLVTGSLHVGDTLRLLKK"

4078..4106

/note="exon predicted by xgrail, quality marginal"

<4481..>6035

/gene="T22K18.2"

/note="predicted by gensecan+"

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/note="hypothetical protein"

/codon_start=1

/protein_id="AA04409.1"

/db_xref="GI:6143862"

/translation="MKKPSLRFQIIIVLSPTTGRVGNLRRESPPKIAFADH
 FGEDTWDGEGDVNSVNSAVLDAETPDVYLDGVYANNIAIQMSLFDKAI
 SPTDRGI PMATLIFGNHDDASFWMLPMLSSSGIPPLRCPASDDDCGTGTRREL
 IOEIKSSNALSYGMI SPKELMPSVNSVYLVBSSDSKSPVALVFLDGGSGSYPV
 ISNAQVEFTKSTLNLYLRIPELIPHLIPSKAKYKAPLMTTRKCVSINERKV
 AOEANGMMRVLENRSSYKAVFGVHNGHLMCCPYKDKMLCFARHNGYGGYGWPRG
 SRLIEISMPFRITKWTIRMEDGSHSEVNLTYD"

complement (6053..6230)

/note="exon predicted by xgrail, quality good_shadowexon"

/complement (<6468..>8553)

/gene="T22K18.3"

/note="similar to RecA protein GB:BA78779
 (Rhodospseudomonas palustris)"

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/gene="T22K18.3"

CDS

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/gene="T22K18.3"

/codon_start=1

/product="putative RecA protein"

/protein_id="AA04410.1"

/db_xref="GI:6143863"

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 ASDCELDVDPDRKVAEKDTALHLASQSGPDFDSKLSIORFYRKRRVSITGSL
 NDLALGVGLPKGMVVEVGEKSGKTTALHIIKEAKQIGCGCAVLDABEAMDPST
 AESIGVNTBELISRPSSAEKRLNVDVLTSGSDVLYVDSVALAQCCELDAPVGE
 RYRDTQSRIMTQALKRIHYSVGSQTLVFLNQVSHVSKNMFPHASEVTGGRALP
 FHAIRLMKIRTKGLIKTANKYGLNVCQVYKXKLAPKKSSELGIHGHGQYVEREV
 LELACEGVILREGTSTYFIEGEGKAAEKLVENEALDTVAAILRNQLFKM"

complement (8596..8676)

/note="exon predicted by xgrail, quality good_shadowexon"

/complement (8803..8900)

/rpt_family="TAAAAn"

/complement (8805..8840)

/rpt_family="POLY_A"

8974..9235

/note="exon predicted by xgrail, quality excellent"

9303..9423

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complement (9461..9610)

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/note="unknown protein"

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/db_xref="GI:6143864"

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 NAIIRQPOSPVASTESVSLVLAASQASSVSQRLDLAMETKTYFPRFDSST
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 LAEYLFQKTIKEKEMETTPVTVTRKQSVGEKEMETTPVITSKXQONQWRGFWPS
 KYGSLNPLKPDSSVKIQQVPRKIVAVAFSGVTDTEIBRRRRELRALONDKKFFVR
 DGVSPVAGVNPETLPRMRNVEGLVENKED"

complement (12526..12557)

/note="exon predicted by xgrail, quality marginal_shadowexon"

complement (12647..13454)

/gene="T22K18.5"

/note="predicted by gensecan+, multiple est matches"

complement (12647..13454)

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/complement (12861..13364)

/gene="T22K18.5"

/note="unknown protein"

/codon_start=1

/protein_id="AA04412.1"

/db_xref="GI:6143865"

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 CHHLPARKLIGLTYLLPOEITNSIIGMKTKMKVAFAPBEVEKEQEDRLTDCDN
 TREKTKGVVKKVAVSQLEKTLQGSVHEMVYRTLAKQLCHDDDECHKEGMRPL
 DGIPEPD"

complement (13084..13157)

/rpt_family="(GAA)n"

/complement (13387..13465)

/rpt_family="(CAAA)n"

13913..13972

/note="exon predicted by xgrail, quality good_shadowexon"

complement (14089..14181)

/note="exon predicted by xgrail, quality marginal"

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misc_feature

gene

mRNA

CDS

misc_feature

gene

mRNA

misc_feature

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 Best Local Similarity 90.0%; Pred. No. 3.3e+02;
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 CTGATGCCAAGCAGCAAC 20
 |||||
 DB 19925 CTGATGCCAAGCAGCAAC 19906

RESULT 10

AC007475

LOCUS AC007475 173613 bp DNA linear INV 28-FEB-2001
 DEFINITION Drosophila melanogaster, chromosome 2R, region 49A-49B, BAC clone
 BACR04521, complete sequence.

ACCESSION

AC007475

VERSION

AC007475.7

KEYWORDS

HTG

SOURCE

ORGANISM

Drosophila melanogaster (fruit fly)
 Drosophila melanogaster
 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 Ephydroidea; Drosophilidae; Drosophila.

1 (bases 1 to 173613)
 Celniker,S.E., Adams,M.D., Kronmiller,B., Tyler,D., Wan,K.H.,
 Holt,R.A., Evans,C.A., Gocayne,J.D., Amanatides,P.G., Brandon,R.C.,
 Rogers,Y., An,H., Baldwin,D., Banzon,J., Beeson,K.Y., Buesam,D.A.,
 Carlson,J.W., Center,A., Chape,M., Davenport,L.B., Dietz,S.M.,
 Dodson,K., Dorsett,V., Doup,L.E., Doyle,C., Dreanek,D., Farfan,D.,
 Ferreira,S., Frise,E., Galle,R.F., Garg,N.S., George,R.A.,
 Gonzalez,M., Houck,T., Hoskins,R.A., Hoslin,D., Howland,T.J.,
 Ibegwam,C., Jalili,M., Kruse,D., Li,P., Mattei,B., Moshrefi,A.,
 McIntosh,T.C., Moy,M., Murphy,B., Nelson,C., Nelson,K.A., Nunoo,J.,
 Pacleb,J., Paragas,V., Park,S., Patel,S., Pfeiffer,B., Scheeler,F.,
 Shuennanavong,S., Pittman,G.S., Puri,V., Richards,S., Scheeler,F.,
 Stapleton,M., Strong,R., Svirskaas,R., Tector,C., Williams,S.M.,
 Zaveri,J.S., Smith,H.O., Rubin,G.M. and Venter,J.C.

Sequencing of Drosophila chromosome 2R, region 49A-49B
 Unpublished

2 (bases 1 to 173613)
 Celniker,S.E., Abbayant,A., Arcaina,T.T., Baxter,E., Blazek,R.G.,
 Butenoff,C., Champe,M., Chavez,C., Chew,M., Ciesiolka,L.,
 Doyle,C.M., Farfan,D.E., Galle,R., George,R.A., Harris,N.L.,
 Hoskins,R.A., Houston,K.A., Hummasti,S.R., Karra,K., Kearney,L.,
 Kim,E., Lee,B., Lewis,S., Li,P., Lomolan,M.A., Mazda,P.,
 Moshrefi,A.R., Moshrefi,M., Nixon,K., Pacleb,J.M., Park,S.,
 Pfeiffer,B., Poon,L., Sequeira,A., Sethi,H., Sutr,E.,
 Svirskaas,R.R., Wan,K.H., Weinburg,T., Zhang,R., Zieran,L.L. and
 Rubin,G.M.

Direct Submission
 Submitted (05-MAY-1999) Drosophila Genome Center, Lawrence Berkeley
 Laboratory, MS 64-121, Berkeley, CA 94720, USA
 On Feb 28, 2001 this sequence version replaced gi:6951978.

Sequence submitted by:
 Lawrence Berkeley National Laboratory, MS 64-121
 Berkeley, CA 94720

This sequence was assembled using end sequences from a whole genome
 shotgun and from subclones of this BAC and its neighboring clones.
 For further information about this sequence, including its location
 and relationship to other sequences, please visit our sequence
 archive Web site (<http://www.fruitfly.org/sequence/>) or send email
 to bdgs@fruitfly.berkeley.edu.

location/Qualifiers
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 /db_xref="taxon:7227"
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 /clone="BACR04521 (DS92)"
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 Drosophila melanogaster BAC library, partial EcORI in

BASE COUNT 48071 a 37844 c 38273 g 49425 t
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Query Match 84.0%; Score 16.8; DB 3; Length 173613;
 Best Local Similarity 90.0%; Pred. No. 3.5e+02;
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 CTGATGCCAAGCAGCAAC 20
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 DB 25802 CTGATGCCAAGCAGCAAC 25821

RESULT 11

AC007474

LOCUS AC007474 192763 bp DNA linear INV 28-FEB-2001
 DEFINITION Drosophila melanogaster, chromosome 2R, region 49A-49B, BAC clone
 BACR14L19, complete sequence.

ACCESSION

AC007474

VERSION

AC007474.5

KEYWORDS

HTG

SOURCE

ORGANISM

Drosophila melanogaster (fruit fly)
 Drosophila melanogaster
 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 Ephydroidea; Drosophilidae; Drosophila.

1 (bases 1 to 192763)
 Celniker,S.E., Adams,M.D., Kronmiller,B., Tyler,D., Wan,K.H.,
 Holt,R.A., Evans,C.A., Gocayne,J.D., Amanatides,P.G., Brandon,R.C.,
 Rogers,Y., An,H., Baldwin,D., Banzon,J., Beeson,K.Y., Buesam,D.A.,
 Carlson,J.W., Center,A., Chape,M., Davenport,L.B., Dietz,S.M.,
 Dodson,K., Dorsett,V., Doup,L.E., Doyle,C., Dreanek,D., Farfan,D.,
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 Pacleb,J., Paragas,V., Park,S., Patel,S., Pfeiffer,B.,
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 Stapleton,M., Strong,R., Svirskaas,R., Tector,C., Williams,S.M.,
 Zaveri,J.S., Smith,H.O., Rubin,G.M. and Venter,J.C.

Sequencing of Drosophila chromosome 2R, region 49A-49B
 Unpublished

2 (bases 1 to 192763)
 Celniker,S.E., Abbayant,A., Arcaina,T.T., Baxter,E., Blazek,R.G.,
 Butenoff,C., Champe,M., Chavez,C., Chew,M., Ciesiolka,L.,
 Doyle,C.M., Farfan,D.E., Galle,R., George,R.A., Harris,N.L.,
 Hoskins,R.A., Houston,K.A., Hummasti,S.R., Karra,K., Kearney,L.,
 Kim,E., Lee,B., Lewis,S., Li,P., Lomolan,M.A., Mazda,P.,
 Moshrefi,A.R., Moshrefi,M., Nixon,K., Pacleb,J.M., Park,S.,
 Pfeiffer,B., Poon,L., Sequeira,A., Sethi,H., Sutr,E.,
 Svirskaas,R.R., Wan,K.H., Weinburg,T., Zhang,R., Zieran,L.L. and
 Rubin,G.M.

Direct Submission
 Submitted (05-MAY-1999) Drosophila Genome Center, Lawrence Berkeley
 Laboratory, MS 64-121, Berkeley, CA 94720, USA
 On Feb 28, 2001 this sequence version replaced gi:5670617.

Sequence submitted by:
 Lawrence Berkeley National Laboratory, MS 64-121
 Berkeley, CA 94720

This sequence was assembled using end sequences from a whole genome
 shotgun and from subclones of this BAC and its neighboring clones.
 For further information about this sequence, including its location
 and relationship to other sequences, please visit our sequence
 archive Web site (<http://www.fruitfly.org/sequence/>) or send email
 to bdgs@fruitfly.berkeley.edu.

location/Qualifiers
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FEATURES

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 Drosophila melanogaster BAC library, partial EcORI in

FEATURES

source

1..192763
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/clone="BAC141L19 (D591)"
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Best Local Similarity 90.0%; Pred. No. 3.5e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Db      150079 CTGATGCCCAACGAGCAAC 150098

RESULT 12
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LOCUS      Drosophila melanogaster, *** SEQUENCING IN PROGRESS ***
AC020286
AC020286.1 GI:6664611
HTG; HTGS_PHASE2.
Drosophila melanogaster (fruit fly)
KEYWORDS      Drosophila melanogaster
SOURCE      Eukaryote; Metazoa; Arthropoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 194634)
REFERENCE
AUTHORS      Adams,M. and Venter,J.C.
TITLE      Direct Submission
JOURNAL      Submitted (30-DEC-1999) Celera Genomics, 45 West Gude Drive,
Rockville, MD, USA
COMMENT      This sequence was identified as CDM:1021263 by the submitter.
For more information on this record e-mail to fly@celera.com.
* NOTE: This is a 'working draft' sequence.
* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.
FEATURES
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/db_xref="taxon:7227"
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Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 CTGATGCCCAACGAGCAAC 20
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Db      58864 CTGATGCCCAACGAGCAAC 58845

RESULT 13
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LOCUS      Rattus norvegicus clone CH230-334A14, *** SEQUENCING IN PROGRESS
AC109049
AC109049.4 GI:23101194
HTG; HTGS_PHASE1; HTGS_DNAFF; HTGS_ENRICHED.
KEYWORDS      Rattus norvegicus (Norway rat)
SOURCE      Rattus norvegicus
ORGANISM      Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
1 (bases 1 to 206732)
REFERENCE
AUTHORS      Muzny,D.,Marle,M.,Metzker,M.,Lee,A.,Abramson,S.,Adams,C.,Alder,J.,
Allen,C.,Allen,H.,Alsbrooks,S.,Amin,A.,Angiano,D.,

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Anylabechi,V.,Aoyagi,A.,Ayodeji,M.,Baca,E.,Baden,H.,
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Biswalo,K.,Blair,J.,Blankenburg,K.,Blyth,P.,Brown,M.,
Bryan,N.,Bunay,C.,Burch,P.,Burrell,K.,Calderon,E.,
Cardenas,V.,Carter,K.,Cavares,I.,Caesar,H.,Center,A.,
Chacko,J.,Chavez,D.,Chen,G.,Chen,R.,Chen,Y.,Chen,Z.,Chu,J.,
Cleveland,C.,Cockrell,R.,Cox,C.,Coyle,M.,Crete,A.,D'Souza,L.,
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Diaper,H.,Dugan-Rocha,S.,Dunn,A.,Durbin,K.,Duvall,B.,Eaves,K.,
Egan,A.,Escotto,M.,Eugene,C.,Evans,C.A.,Falls,T.,Fan,G.,
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Liu,J.,Liu,W.,Liu,Y.,London,P.,Longacre,S.,Lopez,J.,
Lorenzheva,L.,Loulaged,H.,Lozada,R.J.,Lu,X.,Ma,J.,
Maheshwari,M.,Mahindaratne,M.,Mahmoud,M.,Malloy,K.,Mangum,A.,
Mangum,B.,Mapa,P.,Martin,K.,Martin,R.,Martinez,E.,
Mawhinney,S.,McLeod,M.P.,McNeill,T.Z.,Meenan,E.,
Milosavljevic,A.,Miner,G.,Minja,E.,Montemayor,J.,Moore,S.,
Morgan,M.,Morris,K.,Morris,S.,Munidas,M.,Murphy,M.,Nair,L.,
Nankervis,C.,Neal,D.,Newton,N.,Nguyen,N.,Norris,S.,
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Plopper,F.,Polindexter,A.,Popovic,D.,Primus,E.,Pul,L.,
Puzo,M.,Quiroz,J.,Rachlin,E.,Reeves,K.,Reigler,M.A.,Reigh,R.,
Reilly,B.,Reilly,M.,Ren,Y.,Reuter,M.,Richards,S.,Riggs,F.,
Rives,C.,Rodkey,T.,Rojas,A.,Rose,M.,Rose,R.,Ruiz,S.J.,
Sanders,W.,Savery,G.,Scherer,S.,Scott,G.,Shasman,S.,Shen,H.,
Shetty,J.,Shvartsbryn,A.,Sisson,I.,Sitter,C.D.,Snares,D.,
Sneed,A.,Sodergren,E.,Song,X.-Z.,Sorelle,A.,Taber,P.,Taylor,C.,
Steinle,M.,Strong,R.,Sutton,A.,Swatek,A.,Tabor,Z.,Usmani,K.,
Taylor,T.,Thomas,N.,Thomas,S.,Thigley,A.,Walker,B.,Wang,J.,
Valas,R.,Vera,V.,Villasana,D.,Waldron,L.,Walker,B.,Wang,J.,
Wang,O.,Wang,S.,Warren,J.,Warren,R.,Wei,X.,White,F.,
Williams,G.,Willson,R.,Wleczky,R.,Wooden,H.,Worley,K.,
Wright,D.,Wright,R.,Wu,J.,Yakub,S.,Yen,J.,Yoon,L.,Yoon,V.,
Yu,F.,Zhang,J.,Zhou,J.,Zhou,X.,Zhao,S.,Zhou,D.,von
Niederhausern,A.,Weiss,R.,Smith,D.R.,Holt,R.A.,Smith,H.O.,
Weinstock,G. and Gibbs,R.A.
Direct Submission
Unpublished
2 (bases 1 to 206732)
REFERENCE
AUTHORS      Worley,K.C.
TITLE      Direct Submission
JOURNAL      Submitted (03-FEB-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 206732)
REFERENCE
AUTHORS      Rat Genome Sequencing Consortium.
TITLE      Direct Submission
JOURNAL      Submitted (09-OCT-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
On Sep 18, 2002 this sequence version replaced gi:21737800.
The sequence in this assembly is a combination of BAC based reads
and whole genome shotgun sequencing reads assembled using Atlas
(http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig scaffold
in the feature table below represents a scaffold in the Atlas
assembly (a 'contig-scaffold'). Within each contig-scaffold,
individual sequence contigs are ordered and oriented, and separated
by sized gaps filled with Ns to the estimated size. The sequence
may extend beyond the ends of the clone and there may be sequence
contigs within a contig-scaffold that consist entirely of whole
genome shotgun sequence reads. Both end sequences and whole genome
shotgun sequence only contigs will be indicated in the feature

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Table.

----- Genome Center
Center: Baylor College of Medicine
Center code: BCM

Web site: <http://www.hgsc.bcm.tmc.edu/>
Contact: hgsc-help@bcm.tmc.edu

----- Project Information
Center project name: GPNJ
Center clone name: CH230-334A14

----- Summary Statistics

Assembly program: Phrap, version 0.990329

Consensus quality: 181594 bases at least Q40

Consensus quality: 184576 bases at least Q30

Consensus quality: 186555 bases at least Q20

Estimated insert size: 197225; sum-of-coverage estimation

Quality coverage: 5x in Q20 bases; sum-of-coverage estimation

- * NOTE: Estimated insert size may differ from sequence length
- * (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
- * NOTE: This is a 'working draft' sequence. It currently
- * consists of 2 contigs. The true order of the pieces
- * is not known and their order in this sequence record is
- * arbitrary. Gaps between the contigs are represented as
- * runs of N, but the exact sizes of the gaps are unknown.
- * This record will be updated with the finished sequence
- * as soon as it is available and the accession number will
- * be preserved.

1 3973: contig of 3973 bp in length
3974 4073: gap of unknown length
4074 206732: contig of 202659 bp in length.

FEATURES

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site:Mbol

end_sequence:RXAPN07TV"

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/note="wgs contig"

/complement(200587..201453)

/note="clone boundary"

clone end: T7

site:Mbol

end_sequence:RXAPN07TV"

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BASE COUNT 54264 a 40169 c 41232 g 52474 t 18593 others
ORIGIN

Query Match 84.0%; Score 16.8; DB 2; Length 206732;

Best Local Similarity 90.0%; Prid. No. 3.5e+02;

Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CTGATGCCAAGCAGACAC 20
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RESULT 14

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LOCUS Rattus norvegicus clone CH230-94M19, *** SEQUENCING IN PROGRESS

DEFINITION *** 5 unordered pieces.

AC102969

AC102969 7 GI:30522593

KEYWORDS HTG: HTGS PHASE1; HTGS DRAFT; HTGS_ENRICHED.

SOURCE Rattus norvegicus (Norway rat)

ORGANISM Rattus norvegicus

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.

REFERENCE

AUTHORS

1 (bases 1 to 259345)

Muzny, D., Marle, Metzker, M., Lee, Abramson, S., Adams, C., Alder, J.,

Allen, C., Allen, R., Alsbrooks, S., Amis, A., Anguiano, D.,

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Cleveland, C., Cockrell, R., Cox, C., Coyle, M., Crete, A., D'Souza, L.,

Davila, M.L., Davis, C., Davy-Carroll, L., De Anda, C., Dederich, D.,

Delgado, O., Denson, S., Deramo, C., Ding, Y., Dinh, H., Divya, K.,

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Kowals, C., Kraft, C.L., Lebow, H., Levan, J., Lewis, L., Li, Z., Liu, J.,

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Maheshwari, M., Mahindaratne, M., Mahmoud, M., Malloy, K., Mangum, A.,

Mangum, B., Mapa, P., Martin, K., Martin, R., Martinez, E.,

Mawhney, S., McLeod, M.P., McNeill, T.Z., Meenen, E.,

Milosavljevic, A., Miner, G., Minja, E., Montemayor, J., Moore, S.,

Morgan, M., Morris, K., Morris, S., Muntana, M., Murphy, M.,

Nankervis, C., Neal, D., Newton, N., Nguyen, N., Norris, S.,

Nwackelme, O., Okunnu, G., Olamugbesu, A., Pal, S., Parks, K.,

Pasternak, S., Paul, H., Perez, A., Perez, L., Plank, C.,

Plopper, F., Poudexter, A., Popovic, D., Primus, E., Pu, L., L.,

Puazo, M., Quiroz, J., Rachlin, E., Reeves, K., Regier, M.A., Reigh, R.,

Reilly, B., Reilly, M., Ren, Y., Reuter, M., Richards, S., Riggs, F.,

River, C., Rodkey, T., Rojas, A., Rose, M., Rose, R., Ruiz, S., J.,

Sanders, W., Savary, G., Scherer, S., Scott, G., Sheltman, S., Shen, H.,

Shetty, J., Shvartsbeyn, A., Sison, I., Sitter, C.D., Smajls, D.,

Shed, A., Sodergren, E., Song, X.-Z., Sorelle, R., Soza, J.,

Steinle, M., Strong, R., Sutton, A., Svatek, A., Taber, P., Taylor, C.,

Taylor, T., Thomas, N., Thomas, S., Tingay, A., Trejos, Z., Umanal, K.,

Valas, R., Vera, V., Villaseana, D., Waldron, L., Walker, B., Wang, J.,

Wang, Q., Wang, S., Warren, J., Warren, R., Wei, X., White, F.,

Williams, G., Willson, R., Wleczek, R., Woden, H., Wotley, K.,

Wright, D., Wright, R., Wu, J., Yakub, S., Yen, U., Yoon, V.,

Yu, F., Zhang, J., Zhou, X., Zhou, S., Zhao, S., Dunn, D., von

Niederhauser, A., Weiss, R., Smith, D.R., Holt, R.A., Smith, H.O.,

Weinstock, G. and Gibbs, R.A.

Direct Submission

Unpublished

2 (bases 1 to 259345)

Worley, K.C.

Direct Submission

Submitted (24-NOV-2001) Human Genome Sequencing Center, Department

of Molecular and Human Genetics, Baylor College of Medicine, One

Baylor Plaza, Houston, TX 77030, USA

3 (bases 1 to 259345)

Rat Genome Sequencing Consortium.

Submitted (10-MAY-2003) Human Genome Sequencing Center, Department

of Molecular and Human Genetics, Baylor College of Medicine, One

Baylor Plaza, Houston, TX 77030, USA

On May 10, 2003 this sequence version replaced gi:24819627.

The sequence in this assembly is a combination of BAC based reads

and whole genome shotgun sequencing reads assembled using Atlas

(<http://www.hgsc.bcm.tmc.edu/projects/rat/>). Each contig described

in the feature table below represents a scaffold in the Atlas

assembly (a 'contig-scaffold'). Within each contig-scaffold, and separated

by sized gaps filled with Ns to the estimated size. The sequence

may extend beyond the ends of the clone and there may be sequence

contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence only contigs will be indicated in the feature table.

----- Genome Center
Center: Baylor College of Medicine

Center code: BCM

Web site: <http://www.hgsc.bcm.tmc.edu/>

Contact: hgsc-help@bcm.tmc.edu

----- Project Information

Center project name: G60G

Center clone name: CH230-94M19

----- Summary Statistics

Assembly program: Atlas 3.0i

Consensus quality: 242269 bases at least Q40

Consensus quality: 247151 bases at least Q30

Consensus quality: 249910 bases at least Q20

Estimated insert size: 260613; sum-of-contigs estimation

Quality coverage: 6x in Q20 bases; sum-of-contigs estimation

* NOTE: Estimated insert size may differ from sequence length

* (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html)

* NOTE: This sequence may represent more than one clone.

* NOTE: This is a 'working draft' sequence. It currently

* consists of 5 contigs. The true order of the pieces

* is not known and their order in this sequence record is

* arbitrary. Gaps between the contigs are represented as

* runs of N, but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence

* as soon as it is available and the accession number will

* be preserved.

* 1 248466: contig of 248466 bp in length

* 248467 248566: gap of unknown length

* 248567 254507: contig of 5941 bp in length

* 254508 254607: gap of unknown length

* 254608 256455: contig of 1848 bp in length

* 256456 256555: gap of unknown length

* 256556 258160: contig of 1605 bp in length

* 258161 258260: gap of unknown length

* 258261 259345: contig of 1085 bp in length.

* Location/Qualifiers

1. 259345

/organism="Rattus norvegicus"

/mol_type="Genomic DNA"

/db_xref="taxon:10116"

/clone="CH230-94M19"

1. 3071

/note="wgs contig"

complement(245699..246677)

/note="clone boundary"

clone end: T7

site: EORI

end sequence: BH355461"

251214..254507

/note="wgs end extension"

clone end: T7"

BASE COUNT 79986 a 53670 c 51512 g 66827 t 7350 others

ORIGIN

Query Match 84.0%; Score 16.8; DB 2; Length 259345;

Best Local Similarity 90.0%; Pred. No. 3.5e+02;

Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CTGATCGCAACGAGCAGAC 20

|||||

DB 204951 CTGATCACCACACGACAC 204970

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ACCESSION

AC103330

VERSION

GI:30580846

KEYWORDS

HTGS, HTGS_PHASE1, HTGS_DRAFT, HTGS_FULLTOP.

SOURCE

Rattus norvegicus (Norway rat)

ORGANISM

Rattus norvegicus

REFERENCE

AUTHORS

1 (bases 1 to 261157)

Murny, D. Marie, Metzker, M. Lee, Abramson, S., Adams, C., Alder, J.,

Allen, C., Allen, H., Albrooks, S., Amin, A., Anguiano, D.,

Anyalebechi, V., Aoyagi, A., Ayodeji, M., Baca, E., Baden, H.,

Baldwin, D., Bandaranaike, D., Barber, M., Barnstead, M., Benahmed, F.,

Biswal, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M.,

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Cardenas, V., Carter, K., Cavazos, I., Caesar, H., Center, A.,

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Egan, A., Escotto, M., Eugene, C., Evans, C.A., Falls, T., Fan, G.,

Fernandez, S., Finley, M., Flagg, N., Forbes, L., Foster, M., Foster, P.,

Frieder, C.M., Gabisi, A., Ganta, R., Garcia, A., Garner, T., Garza, M.,

Gebregiorgis, E., Geer, A., Gill, R., Grady, M., Guerra, M., Guevara, W.,

Gunaratne, P., Haaland, W., Hamill, C., Hamilton, C., Hamilton, K.,

Harvey, Y., Havlak, P., Hawes, A., Henderson, N., Hernandez, J.,

Hernandez, R., Hines, S., Hladun, S.L., Hodgson, A., Hognes, M.,

Hollins, B., Howells, S., Huliy, S., Hume, J., Idlebird, D., Jackson, A.,

Jackson, L., Jacob, L., Jiang, H., Johnson, B., Johnson, R., Jolivet, A.,

Kapathy, S., Kelly, S., Kelly, S., Khan, Z., King, L., Kovar, C.,

Kowis, C., Kraft, C.L., Lebow, H., Levan, J., Lewis, L., Li, Z., Liu, J.,

Liu, J., Liu, W., Liu, Y., London, P., Longacre, S., Lopez, J.,

Lorenshewa, L., Louissege, H., Lozano, R.J., Lu, X., Ma, J.,

Maheshwari, M., Mahindratne, M., Mahmoud, M., Malloy, K., Mangum, A.,

Mangum, B., Mapa, P., Martin, K., Martin, R., Martinez, E.,

Mawney, S., McLeod, M.P., McNeill, T.Z., Meenen, E.,

Milosavljevic, A., Milner, G., Minja, E., Montemayor, J., Moore, S.,

Morgan, M., Morris, K., Morris, S., Mundaasa, M., Murphy, M., Nair, L.,

Nankervyl, C., Neal, D., Newton, N., Nguyen, N., Norris, S., Parks, K.,

Nwackeme, O., Okwodu, G., Olarnpungoon, A., Pal, S., Parks, K.,

Pasternak, S., Paul, H., Perez, A., Perez, L., Pfannkuch, C.,

Plopper, F., Polidexter, A., Popovic, D., Primus, E., Pu, L.,

Punzo, M., Quiroz, J., Rachlin, E., Reeves, K., Reiter, M.A., Reigh, R.,

Reilly, B., Rodkey, T., Rojas, A., Rose, M., Rose, R., Ruiz, S., Riggs, F.,

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Sanders, W., Savary, G., Scherer, S., Scott, G., Shatman, S., Shen, H.,

Shetty, J., Shvartbeyn, A., Sisson, I., Sitter, C.D., Smajs, D.,

Sneed, A., Sodergren, E., Song, X.-Z., Sorelle, R., Soosa, J.,

Steinle, M., Strong, R., Sutton, A., Svatek, A., Taber, P., Taylor, C.,

Taylor, T., Thomas, N., Thomas, S., Tingey, A., Trejos, Z., Uman, K.,

Valas, R., Vera, V., Villanar, D., Waldron, L., Walker, B., Wang, J.,

Wang, Q., Wang, S., Warren, J., Warren, R., Wei, X., White, F.,

Williams, G., Willison, R., Wleczky, R., Wooden, H., Wotley, K.,

Wright, D., Wright, R., Wu, J., Yakub, S., Yen, J., Yoon, L., Yoon, V.,

Yu, F., Zhang, J., Zhou, J., Zhou, X., Zhao, S., Dunn, D., von

Niederhausen, A., Weiss, R., Smith, D.R., Holt, R.A., Smith, H.O.,

Weinstock, G., and Gibbs, R.A.

Direct Submission

Unpublished

JOURNAL

TITLE

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Submitted (13-MAY-2003) Human Genome Sequencing Center, Department

of Molecular and Human Genetics, Baylor College of Medicine, One

Baylor Plaza, Houston, TX 77030, USA

On May 13, 2003 this sequence version replaced gi:22857506.

The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (<http://www.hgsc.bcm.tmc.edu/projects/rat/>). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence only contigs will be indicated in the feature table.

Genome Center

Center: Baylor College of Medicine

Center code: BCM

Web site: <http://www.hgsc.bcm.tmc.edu/>

Contact: hgsc-help@bcm.tmc.edu

----- Project Information

Center project name: GLAH

Center clone name: CH230-177K18

----- Summary Statistics

Assembly program: Atlas 3.0;

Consensus quality: 247708 bases at least Q40

Consensus quality: 250022 bases at least Q30

Consensus quality: 251823 bases at least Q20

Estimated insert size: 259364; sum-of-contigs estimation

Quality coverage: 9x in Q20 bases; sum-of-contigs estimation

* NOTE: Estimated insert size may differ from sequence length
 * (see http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html)
 * NOTE: This sequence may represent more than one clone.
 * NOTE: This is a 'working draft' sequence. It currently
 * consists of 7 contigs. The true order of the pieces
 * is not known and their order in this sequence record is
 * arbitrary. Gaps between the contigs are represented as
 * runs of N, but the exact sizes of the gaps are unknown.
 * This record will be updated with the finished sequence
 * as soon as it is available and the accession number will
 * be preserved.

```

1 242048: contig of 242048 bp in length
* 242049 242148: gap of unknown length
* 242149 246131: contig of 3983 bp in length
* 246132 246231: gap of unknown length
* 246232 252340: contig of 6109 bp in length
* 252341 252440: gap of unknown length
* 252441 253496: contig of 1056 bp in length
* 253497 253596: gap of unknown length
* 253597 255683: contig of 2087 bp in length
* 255684 255783: gap of unknown length
* 255784 257688: contig of 1905 bp in length
* 257689 261157: gap of unknown length
* 257789 261157: contig of 3369 bp in length.
Location/Qualifiers
1. 261157

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FEATURES
 source
 1. 261157
 /organism="Rattus norvegicus"
 /mol_type="genomic DNA"
 /db_xref="taxon:10116"
 /clone="CH230-177K18"

mlsc_feature

mlsc_feature

mlsc_feature

mlsc_feature

mlsc_feature

mlsc_feature

mlsc_feature

mlsc_feature

mlsc_feature

BASE COUNT 66925 a 60485 c 60256 g 65490 t 8001 others
 ORIGIN

Query Match 84.0%; Score 16.8; DB 2; Length 261157;
 Best Local Similarity 90.0%; Pred. No. 3.5e+02;

Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CTGATCGCCAAACGAGCAAC 20

Db 134133 CTGATCGCCAGACGAGCAGC 134152

Search completed: February 12, 2004, 04:41:47
 Job time : 591.854 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Comogen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 12, 2004, 01:53:19 ; Search time 105.122 Seconds
(without alignments)
513.582 Million cell updates/sec

Title: US-09-692-077D-15
Perfect score: 20
Sequence: 1 ctgactcgccaacagcgaac 20

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 2552756 seqs, 1349719017 residues

Total number of hits satisfying chosen parameters: 5105512

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: N.GeneSeq_19Jun03.*
2: /SIDSI/gcgdata/geneSeq/geneSeqn-emb1/NA1980.DAT.*
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10: /SIDSI/gcgdata/geneSeq/geneSeqn-emb1/NA1988.DAT.*
11: /SIDSI/gcgdata/geneSeq/geneSeqn-emb1/NA1989.DAT.*
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26: /SIDSI/gcgdata/geneSeq/geneSeqn-emb1/NA2003.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	20	100.0	20	AA199909	Human alpha-2BAR g
2	16.8	84.0	3920	ABL22105	Drosophila melanog
3	16.8	84.0	6990	ABL22104	Drosophila melanog
4	15.8	79.0	277	ABX25006	Human GDP-mannose
5	15.8	79.0	1976	ABX22622	Human GDP-mannose
6	15.8	79.0	5786	AA529976	Human lung antigen
7	15.8	79.0	47999	AA52898	Human tweety homol
8	15.8	79.0	1082138	AAF22305	Arabidopsis thailia

C	9	15.4	77.0	543	24	ABN68569
C	10	15.4	77.0	534720	19	AAV30458
C	11	15.4	77.0	536165	19	AAV30459
C	12	15.2	76.0	144	24	ABO91593
C	13	15.2	76.0	309	24	ABO91594
C	14	15.2	76.0	705	24	ABO65658
C	15	15.2	76.0	1281	25	ABT18455
C	16	15.2	76.0	1284	25	ABT19049
C	17	15.2	76.0	1359	24	ABZ66820
C	18	15.2	76.0	1359	24	ABZ66820
C	19	15.2	76.0	1380	23	ABL14339
C	20	15.2	76.0	1525	24	ABQ44152
C	21	15.2	76.0	1525	24	ABQ44153
C	22	15.2	76.0	1525	24	ABQ45082
C	23	15.2	76.0	1525	24	ABQ45083
C	24	15.2	76.0	1586	21	AA45525
C	25	15.2	76.0	1586	21	AA45525
C	26	15.2	76.0	1586	21	AA45525
C	27	15.2	76.0	2036	23	ABL01847
C	28	15.2	76.0	2193	23	AA553007
C	29	15.2	76.0	2888	23	ABL02530
C	30	15.2	76.0	3266	23	ABL01889
C	31	15.2	76.0	3281	25	ABT17861
C	32	15.2	76.0	3907	23	ABL14338
C	33	15.2	76.0	4779	22	AA529952
C	34	15.2	76.0	6080	23	ABL01846
C	35	15.2	76.0	7874	20	AA520568
C	36	15.2	76.0	8189	23	ABL01888
C	37	15.2	76.0	1664976	19	AAV21209
C	38	15	75.0	1356	23	AA594178
C	39	15	75.0	2416	23	ABL06847
C	40	15	75.0	2943	23	AA586718
C	41	15	75.0	3681	23	ABL06346
C	42	15	75.0	3963	23	AA579164
C	43	14.8	74.0	5379	23	ABL06846
C	44	14.8	74.0	180	14	AAQ4914
C	45	14.8	74.0	304	21	AA10249
C	46	14.8	74.0	391	25	ABX51029

ALIGNMENTS

RESULT 1
ID AA199909 strand: DNA; 20 BP.
AC AA199909;
XX
XX
DT 18-FEB-2002 (first entry)
XX
DE Human alpha-2BAR genotyping PCR primer SEQ ID NO 15.
XX
XX Human; genotyping; alpha-2B; alpha-2A; alpha-2C; adrenergic receptor;
XX polynucleotide site; allelic variant; cardiovascular disease;
XX central nervous system disease; adenylyl cyclase; MAP kinase activity;
XX phosphorylation; inositol phosphate; alpha-2BAR; PCR primer; ss.
XX
XX Homo sapiens.
XX
XX WO200179561-A2.
XX
XX
PD 25-OCT-2001.
XX
XX
PF 17-APR-2001; 2001WO-US12575.
XX
XX
PR 17-APR-2000; 2000US-0551744.
PR 10-AUG-2000; 2000US-0636259.
PR 19-OCT-2000; 2000US-0692077.
XX
XX (LIGG/) LIGGETT S B.
PA (SMAL/) SMALL K M.
XX
XX Liggett SB, Small KM;

Streptococcus poly
Rhizobium species
Rhizobium species
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Arabidopsis thailia
Aspergillus fumiga
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Drosophila melanog
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Enterococcus faeca
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Aspergillus fumiga
Drosophila melanog
Human lung antigen
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Polynucleotide seq
Drosophila melanog
Methanococcus jann
DNA encoding novel
Drosophila melanog
DNA encoding novel
Drosophila melanog
DNA encoding novel
Drosophila melanog
Cytochrome P450 ho
Human secreted pro
Bovine EST associa

XX WPI; 2001-611728/70.
 DR Genotyping an alpha-2B, 2A, or 2C adrenergic receptor gene useful for
 XX determining whether an individual is at increased risk of developing a
 PT disease associated with the corresponding receptor comprises detecting
 PT a polymorphic site -
 XX
 XX Claim 10; Page 112; 163pp; English.
 PS
 XX The invention relates to genotyping an alpha-2B, 2A, or 2C adrenergic
 CC receptor gene (I)-(III) by detecting a polymorphic site, comprising:
 CC (a) obtaining a sample having a polynucleotide encoding an alpha-2B,
 CC alpha2A or alpha2C or fragment or complement of; and
 CC (b) detecting a polymorphic site comprising nucleotide positions 901-909
 CC of (I), a site comprising cytosine or guanine at position 753 of (IIIV)
 CC or a site comprising (A) (ggggggggggcg) or (B) (ggggggggcgag) at
 CC positions 961-972 of (III). The method may be used for genotyping an
 CC alpha2B, alpha2A or alpha2C receptor gene and further used to determine
 CC whether an individual is at increased risk of developing a disease
 CC associated with alpha2B, alpha2A or alpha2, comprising detecting a
 CC polymorphic site which correlate to disease selected from cardiovascular
 CC disease, central nervous system disease and combinations of these. In
 CC addition, the technique may be used to predict an individual's response
 CC to an alpha2B, alpha2A, or alpha2C agonist (e.g. epinephrine,
 CC norepinephrine, clonidine, oxymetazoline, guanabenz, UK14304, BHT933 and
 CC combinations of these) or antagonist (e.g. yohimbine, prazosin, ARC 239,
 CC rauwolfine, idazoxan, tolazoline, phenolamine and combinations of
 CC these) by detecting the polymorphic site and correlating the site to a
 CC predetermined response (where the response is correlated to adenylyl
 CC cyclase, MAP kinase activity, phosphorylation or inositol phosphate
 CC levels). The present sequence is that of a human alpha-2BAR PCR primer,
 CC useful for the genotyping methods of the invention.
 CC
 XX Sequence 20 BP; 7 A; 7 C; 4 G; 2 T; 0 other;
 SQ
 Query Match 100.0%; Score 20; DB 23; Length 20;
 Best Local Similarity 100.0%; Pred. No. 0.82; Mismatches 0; Gaps 0;
 Matches 20; Conservative 0; Indels 0;
 Oy 1 CTGATCGCCAAACGAGCAAC 20
 Db 1 CTGATCGCCAAACGAGCAAC 20
 RESULT 2
 ABL22105
 ID ABL22105 standard; DNA; 3920 BP.
 XX
 AC ABL22105;
 XX
 DT 26-MAR-2002 (first entry)
 XX
 DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 17788.
 XX
 KW Drosophila; developmental biology; cell signalling; insecticide;
 KM pharmaceutical; gene; ds.
 XX
 OS Drosophila melanogaster.
 XX
 PN WO200171042-A2.
 XX
 PD 27-SEP-2001.
 XX
 PF 23-MAR-2001; 2001WO-US09231.
 XX
 PR 23-MAR-2000; 2000US-191637P.
 XX
 PR 11-JUL-2000; 2000US-0614150.
 XX
 PA (PEKE) PE CORP NY.
 XX
 PI Venter JC, Adams M, Li PWD, Myers EW;
 XX

DR WPI; 2001-656860/75.
 XX
 XX New isolated nucleic acid detection reagent for detecting 1000 or more
 PT genes from Drosophila and for elucidating cell signalling and cell-cell
 PT interactions -
 PT
 XX
 PS Claim 1; SEQ ID NO 17788; 21pp + Sequence Listing; English.
 XX
 XX The invention relates to an isolated nucleic acid detection reagent
 CC capable of detecting 1000 or more genes from Drosophila. The invention is
 CC useful in developmental biology and in elucidating cell signalling and
 CC cell-cell interactions in higher eukaryotes for the development of
 CC insecticides, therapeutics and pharmaceutical drugs. The invention
 CC discloses genomic DNA sequences (AB101840-AB16175) and the encoded proteins
 CC (ABBS7737-ABBS72072).
 CC The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.
 CC
 XX Sequence 3920 BP; 1053 A; 1007 C; 947 G; 913 T; 0 other;
 SQ
 Query Match 84.0%; Score 16.8; DB 23; Length 3920;
 Best Local Similarity 90.0%; Pred. No. 57;
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 Oy 1 CTGATCGCCAAACGAGCAAC 20
 Db 3432 CTGATCGCCAAACGAGCAAC 3451
 RESULT 3
 ABL22104/c
 ID ABL22104 standard; DNA; 6990 BP.
 XX
 AC ABL22104;
 XX
 DT 26-MAR-2002 (first entry)
 XX
 DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 17785.
 XX
 KW Drosophila; developmental biology; cell signalling; insecticide;
 KM pharmaceutical; gene; ds.
 XX
 OS Drosophila melanogaster.
 XX
 PN WO200171042-A2.
 XX
 PD 27-SEP-2001.
 XX
 PF 23-MAR-2001; 2001WO-US09231.
 XX
 PR 23-MAR-2000; 2000US-191637P.
 XX
 PR 11-JUL-2000; 2000US-0614150.
 XX
 PA (PEKE) PE CORP NY.
 XX
 PI Venter JC, Adams M, Li PWD, Myers EW;
 XX
 DR WPI; 2001-656860/75.
 XX
 XX New isolated nucleic acid detection reagent for detecting 1000 or more
 PT genes from Drosophila and for elucidating cell signalling and cell-cell
 PT interactions -
 PT
 XX
 PS Claim 1; SEQ ID NO 17785; 21pp + Sequence Listing; English.
 XX
 XX The invention relates to an isolated nucleic acid detection reagent
 CC capable of detecting 1000 or more genes from Drosophila. The invention is
 CC useful in developmental biology and in elucidating cell signalling and
 CC cell-cell interactions in higher eukaryotes for the development of
 CC insecticides, therapeutics and pharmaceutical drugs. The invention
 CC discloses genomic DNA sequences (AB16176-AB130511), expressed DNA
 CC

CC sequences (ABU01840-ABL16175) and the encoded proteins
CC (AB573737-AB572072).
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pat_sequences.

XX Sequence 6990 BP; 1907 A; 1513 C; 1586 G; 1984 T; 0 other;

Query Match 84.0%; Score 16.8; DB 23; Length 6990;
Best Local Similarity 90.0%; Pred. No. 60;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CTGATGCCCAACGAGCAAC 20
Db 1624 CTGATGCCCAACGAGCAAC 1605

RESULT 4

ABX25006/c
ID ABX25006 standard; cDNA; 277 BP.

AC ABX25006;

DT 11-FEB-2003 (first entry)

DE Human GDP-mannose 4,6-dehydratase (GM4,6D) DNA #7063.

XX Human; GDP-mannose 4,6-dehydratase; GM4,6D; gene; ss; inflammation;
KW cellular fucosylation; glycoconjugate fucosylation; transplant rejection;
KW arthritis; asthma; sepsis; reperfusion injury; stroke; infection;
KW complex carbohydrate; gene replacement therapy; immunosuppressive;
KW antiinflammatory; antiarthritic; antibacterial; cerebroprotective;
KW antiaesthetic; vasotropic.

OS Homo sapiens.

PN US2002110548-A1.

PD 15-AUG-2002.

PF 11-JUN-2001; 2001US-0878574.

PR 22-NOV-1996; 96US-0753233.

PR 03-DEC-1997; 97US-0984246.

PR 09-SEP-1998; 98US-0149674.

PR 14-JUN-1999; 99US-0333177.

PA (GENY) GENETICS INST INC.

PI Sullivan F, Kriz R, Kumar R;

DR WPI; 2003-066673/06.

XX New composition comprising GDP-mannose 4,6-dehydratase (GM4,6D)
XX peptide, for manufacturing complex carbohydrates, or as targets for
XX screening GM4,6D antagonists for treating e.g. arthritis, or transplant
XX rejection

PS Disclosure; SEQ ID NO 7065; 6pp; English.

XX The invention relates to a composition comprising a human GDP-mannose
XX 4,6-dehydratase (GM4,6D) peptide. The peptide is useful for identifying
XX GM4,6D inhibitors, GM4,6D inhibitors are useful for reducing inflammation
XX in a mammalian subject and for treating or ameliorating diseases affected
XX by the level of cellular fucosylation or diseases affected by the
XX fucosylation of glycoconjugates. These diseases include arthritis,
XX transplant rejection, asthma, sepsis, reperfusion injury, stroke or
XX infection. The GM4,6D peptide or a polynucleotide encoding it is also
XX useful for manufacturing complex carbohydrates and as targets for
XX screening small molecule antagonists of the activity of the enzyme. The
XX polynucleotide is useful in developing an assay for defects in the
XX enzyme, as well as in gene replacement therapy. Sequences
XX ABX17942-ABX17944 and ABX17947-ABX17946 represent DNA molecules encoding

CC human GM4,6D peptides of the invention.
CC Note: The sequence data for this patent did not form part of the printed
CC specification but was obtained in electronic format directly from USPTO
CC at seqdata.uspto.gov/sequence.html.

XX Sequence 277 BP; 89 A; 57 C; 64 G; 67 T; 0 other;

Query Match 79.0%; Score 15.8; DB 25; Length 277;
Best Local Similarity 89.5%; Pred. No. 1.5e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 TGATGCCCAACGAGCAAC 20
Db 277 TGATGCCCAACGAGCAAC 259

RESULT 5

ABX22622
ID ABX22622 standard; cDNA; 1976 BP.

AC ABX22622;

DT 10-FEB-2003 (first entry)

DE Human GDP-mannose 4,6-dehydratase (GM4,6D) DNA #4679.

XX Human; GDP-mannose 4,6-dehydratase; GM4,6D; gene; ss; inflammation;
KW cellular fucosylation; glycoconjugate fucosylation; transplant rejection;
KW arthritis; asthma; sepsis; reperfusion injury; stroke; infection;
KW complex carbohydrate; gene replacement therapy; immunosuppressive;
KW antiinflammatory; antiarthritic; antibacterial; cerebroprotective;
KW antiaesthetic; vasotropic.

OS Homo sapiens.

PN US2002110548-A1.

PD 15-AUG-2002.

PF 11-JUN-2001; 2001US-0878574.

PR 22-NOV-1996; 96US-0753233.

PR 03-DEC-1997; 97US-0984246.

PR 09-SEP-1998; 98US-0149674.

PR 14-JUN-1999; 99US-0333177.

PA (GENY) GENETICS INST INC.

PI Sullivan F, Kriz R, Kumar R;

DR WPI; 2003-066673/06.

XX New composition comprising GDP-mannose 4,6-dehydratase (GM4,6D)
XX peptide, for manufacturing complex carbohydrates, or as targets for
XX screening GM4,6D antagonists for treating e.g. arthritis, or transplant
XX rejection

PS Disclosure; SEQ ID NO 4681; 6pp; English.

XX The invention relates to a composition comprising a human GDP-mannose
XX 4,6-dehydratase (GM4,6D) peptide. The peptide is useful for identifying
XX GM4,6D inhibitors, GM4,6D inhibitors are useful for reducing inflammation
XX in a mammalian subject and for treating or ameliorating diseases affected
XX by the level of cellular fucosylation or diseases affected by the
XX fucosylation of glycoconjugates. These diseases include arthritis,
XX transplant rejection, asthma, sepsis, reperfusion injury, stroke or
XX infection. The GM4,6D peptide or a polynucleotide encoding it is also
XX useful for manufacturing complex carbohydrates and as targets for
XX screening small molecule antagonists of the activity of the enzyme. The
XX polynucleotide is useful in developing an assay for defects in the
XX enzyme, as well as in gene replacement therapy. Sequences
XX ABX17942-ABX17944 and ABX17947-ABX17946 represent DNA molecules encoding
XX human GM4,6D peptides of the invention.

CC Note: The sequence data for this patent did not form part of the printed
CC specification but was obtained in electronic format directly from USPTO
CC at seqdata.uspto.gov/sequence.html.

XX SQ Sequence 1976 BP; 497 A; 477 C; 374 G; 522 T; 106 other;

Query Match 79.0%; Score 15.8; DB 25; Length 1976;
Best local Similarity 85.0%; Pred. No. 1.8e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CTGATCGCAACGACGAC 20
Db 1174 CTGATCGCAACGATCAC 1193

RESULT 6

AAS29976
ID AAS29976 standard; DNA; 5786 BP.

AC AAS29976;

DT 21-NOV-2001 (first entry)

DE Human lung antigen genomic DNA #46.

XX Lung antigen protein; human; mouse; rabbit; goat; horse; cat; dog;
KW chicken; sheep; immunosuppressive; antiallergic; vasotrophic;
KW antihemetic; antiproliferative; cytostatic; cardiant; neuroprotective;
KW cerebroprotective; nocotropic; antibacterial; virucide; fungicide; cancer;
KW ophthalmological; vulnery; gene therapy; autoimmune disease; neoplasm;
KW hyperproliferative disorder; breast; liver; cardiovascular disorder; ds;
KW cerebrovascular disorder; nervous system disorder; bacterial infection;
KW fungal infection; viral infection; ocular disorder; respiratory disorder;
KW gastrointestinal disorder; renal disorder; respiratory disorder;
KW wound healing; skin aging; organ transplantation; food preservative;
KW tissue regeneration; anti-fertility; food additive.

XX Homo sapiens.

XX WO200155303-A2.

PD 02-AUG-2001.

PF 17-JAN-2001; 2001WO-US01301.

XX 31-JAN-2000; 2000US-0179065.
PR 04-FEB-2000; 2000US-0180628.
PR 24-FEB-2000; 2000US-0184664.
PR 02-MAR-2000; 2000US-0186350.
PR 16-MAR-2000; 2000US-0189874.
PR 17-MAR-2000; 2000US-0190076.
PR 18-APR-2000; 2000US-0198123.
PR 19-MAY-2000; 2000US-0205515.
PR 07-JUN-2000; 2000US-0209467.
PR 28-JUN-2000; 2000US-0214886.
PR 30-JUN-2000; 2000US-0215135.
PR 07-JUL-2000; 2000US-0216647.
PR 07-JUL-2000; 2000US-0216860.
PR 11-JUL-2000; 2000US-0217487.
PR 14-JUL-2000; 2000US-0217496.
PR 26-JUL-2000; 2000US-0218290.
PR 26-JUL-2000; 2000US-0220963.
PR 14-AUG-2000; 2000US-0220964.
PR 14-AUG-2000; 2000US-0224518.
PR 14-AUG-2000; 2000US-0224519.
PR 14-AUG-2000; 2000US-0225213.
PR 14-AUG-2000; 2000US-0225214.
PR 14-AUG-2000; 2000US-0225267.
PR 14-AUG-2000; 2000US-0225268.
PR 14-AUG-2000; 2000US-0225270.
PR 14-AUG-2000; 2000US-0225447.
PR 14-AUG-2000; 2000US-0225757.

PR 14-AUG-2000; 2000US-0225758.
PR 14-AUG-2000; 2000US-0225759.
PR 18-AUG-2000; 2000US-0226279.
PR 22-AUG-2000; 2000US-0226681.
PR 22-AUG-2000; 2000US-0226868.
PR 22-AUG-2000; 2000US-0227182.
PR 23-AUG-2000; 2000US-0227009.
PR 30-AUG-2000; 2000US-0228924.
PR 01-SEP-2000; 2000US-0229287.
PR 01-SEP-2000; 2000US-0229343.
PR 01-SEP-2000; 2000US-0229344.
PR 01-SEP-2000; 2000US-0229345.
PR 05-SEP-2000; 2000US-0229509.
PR 05-SEP-2000; 2000US-0229513.
PR 06-SEP-2000; 2000US-0230437.
PR 06-SEP-2000; 2000US-0230438.
PR 08-SEP-2000; 2000US-0231242.
PR 08-SEP-2000; 2000US-0231243.
PR 08-SEP-2000; 2000US-0231244.
PR 08-SEP-2000; 2000US-0231413.
PR 08-SEP-2000; 2000US-0231414.
PR 08-SEP-2000; 2000US-0232080.
PR 12-SEP-2000; 2000US-0232081.
PR 14-SEP-2000; 2000US-0232396.
PR 14-SEP-2000; 2000US-0232397.
PR 14-SEP-2000; 2000US-0232398.
PR 14-SEP-2000; 2000US-0232399.
PR 14-SEP-2000; 2000US-0232400.
PR 14-SEP-2000; 2000US-0232401.
PR 14-SEP-2000; 2000US-0232403.
PR 14-SEP-2000; 2000US-0232404.
PR 21-SEP-2000; 2000US-0232423.
PR 21-SEP-2000; 2000US-0232424.
PR 25-SEP-2000; 2000US-0234997.
PR 25-SEP-2000; 2000US-0234998.
PR 26-SEP-2000; 2000US-0235484.
PR 27-SEP-2000; 2000US-0235834.
PR 27-SEP-2000; 2000US-0235836.
PR 29-SEP-2000; 2000US-0236367.
PR 29-SEP-2000; 2000US-0236367.
PR 29-SEP-2000; 2000US-0236368.
PR 29-SEP-2000; 2000US-0236369.
PR 02-OCT-2000; 2000US-0236802.
PR 02-OCT-2000; 2000US-0237037.
PR 02-OCT-2000; 2000US-0237038.
PR 02-OCT-2000; 2000US-0237039.
PR 13-OCT-2000; 2000US-0237040.
PR 13-OCT-2000; 2000US-0239935.
PR 20-OCT-2000; 2000US-0240960.
PR 20-OCT-2000; 2000US-0241221.
PR 20-OCT-2000; 2000US-0241785.
PR 20-OCT-2000; 2000US-0241786.
PR 20-OCT-2000; 2000US-0241787.
PR 20-OCT-2000; 2000US-0241808.
PR 20-OCT-2000; 2000US-0241809.
PR 01-NOV-2000; 2000US-0244617.
PR 08-NOV-2000; 2000US-0244617.
PR 08-NOV-2000; 2000US-0244674.
PR 08-NOV-2000; 2000US-0244675.
PR 08-NOV-2000; 2000US-0246476.
PR 08-NOV-2000; 2000US-0246477.
PR 08-NOV-2000; 2000US-0246478.
PR 08-NOV-2000; 2000US-0246523.
PR 08-NOV-2000; 2000US-0246524.
PR 08-NOV-2000; 2000US-0246525.
PR 08-NOV-2000; 2000US-0246526.
PR 08-NOV-2000; 2000US-0246527.
PR 08-NOV-2000; 2000US-0246528.
PR 08-NOV-2000; 2000US-0246529.
PR 08-NOV-2000; 2000US-0246532.

Best Local Similarity 89.5%; Pred. No. 1.9e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 2 TGATGCCAATGACGAC 20
Db 818 TTAATGCCAATGACGAC 836

RESULT 7
AADS2898
ID AADS2898 standard; DNA; 47999 BP.

AC AADS2898;

DT 14-MAY-2003 (first entry)

XX Human tweety homologue 2 (TTYH2) gene.

XX Human; tweety homologue 2; TTYH2; therapy; cancer; tumour; cytostatic;

KW diagnostic marker; gene; ds.

XX Homo sapiens.

XX Key Location/Qualifiers
FH CDS 1946..45753

FT /tag= a
FT /product= "Human TTYH2 protein"

FT 1936..2074

FT /tag= b
FT /number= 1

FT 2075..10376

FT /tag= c
FT 10377..10549

FT /tag= d
FT /number= 2

FT 10550..16622

FT /tag= e
FT 16623..16734

FT /tag= f
FT /number= 3

FT 16735..23223

FT /tag= g
FT 23224..23444

FT /tag= h
FT /number= 4

FT 23445..28299

FT /tag= i
FT /number= 1

FT 28300..28395

FT /tag= j
FT /number= 5

FT 28396..28902

FT /tag= k
FT 28903..28975

FT /tag= l
FT /number= 6

FT 28976..35372

FT /tag= m
FT 35373..35442

FT /tag= n
FT /number= 7

FT 35443..35705

FT /tag= o
FT 35706..35761

FT /tag= p
FT /number= 8

FT 35762..36266

FT /tag= q
FT 36267..36359

FT /tag= r
FT /number= 9

FT 36360..36591

FT /tag= s
FT 36592..36684

PR 08-NOV-2000; 2000US-0246610.
PR 08-NOV-2000; 2000US-0246611.
PR 08-NOV-2000; 2000US-0246613.
PR 17-NOV-2000; 2000US-0249207.
PR 17-NOV-2000; 2000US-0249208.
PR 17-NOV-2000; 2000US-0249209.
PR 17-NOV-2000; 2000US-0249210.
PR 17-NOV-2000; 2000US-0249211.
PR 17-NOV-2000; 2000US-0249212.
PR 17-NOV-2000; 2000US-0249213.
PR 17-NOV-2000; 2000US-0249214.
PR 17-NOV-2000; 2000US-0249215.
PR 17-NOV-2000; 2000US-0249216.
PR 17-NOV-2000; 2000US-0249217.
PR 17-NOV-2000; 2000US-0249218.
PR 17-NOV-2000; 2000US-0249244.
PR 17-NOV-2000; 2000US-0249245.
PR 17-NOV-2000; 2000US-0249246.
PR 17-NOV-2000; 2000US-0249265.
PR 17-NOV-2000; 2000US-0249297.
PR 17-NOV-2000; 2000US-0249299.
PR 17-NOV-2000; 2000US-0249300.
PR 01-DEC-2000; 2000US-0250160.
PR 01-DEC-2000; 2000US-0250391.
PR 05-DEC-2000; 2000US-0251030.
PR 05-DEC-2000; 2000US-0251988.
PR 05-DEC-2000; 2000US-0256719.
PR 06-DEC-2000; 2000US-0251479.
PR 08-DEC-2000; 2000US-0251856.
PR 08-DEC-2000; 2000US-0251868.
PR 08-DEC-2000; 2000US-0251869.
PR 08-DEC-2000; 2000US-0251989.
PR 08-DEC-2000; 2000US-0251990.
PR 11-DEC-2000; 2000US-0254097.
PR 05-JAN-2001; 2001US-0259678.
XX
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
XX
PI Rosen CA, Barash SC, Ruben SM;
XX
XX WPI; 2001-457723/49.
XX
PT Isolated polypeptide for treating, preventing and/or prognosing
PT respiratory disorders related to the lung including lung cancers and
PT also for testing and detection e.g. diagnosis -
XX
XX
PS Claim 1; SEQ ID No 240; 507pp; English.
XX
XX Sequences AAS29931-AAS30164 represent genomic DNA molecules, which encode
CC the lung antigen polypeptides of the invention. Lung antigen polypeptides
CC and their associated polynucleotides are useful in the diagnosis,
CC treatment and prevention of various types of disorders in e.g. humans,
CC mice, rabbits, goats, cats, dogs, chickens or sheep. A
CC pathological condition can be determined by detecting the presence or
CC absence of a mutation in a lung antigen polynucleotide. The treatable
CC disorders include autoimmune diseases such as rheumatoid arthritis,
CC hyperproliferative disorders such as neoplasms of the breast or liver,
CC cardiovascular disorders such as cardiac arrest, cerebrovascular
CC disorders such as cerebral ischaemia, nervous system disorders such as
CC Alzheimer's disease, infections caused by bacteria, viruses and fungi,
CC ocular disorders such as corneal infection, endocrine disorders such as
CC premature labour and infertility, gastrointestinal disorders such as
CC Crohn's disease, renal disorders such as glomerulonephritis and
CC respiratory disorders such as asthma and pleurisy. The polypeptides can
CC also be used to aid wound healing, to prevent skin aging due to sunburn,
CC to maintain organs before transplantation, to regenerate tissues and in
CC chemotaxis. The polypeptides can also be used as a food additive or
CC preservative to increase or decrease storage capabilities.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.

Query Match 79.0%; Score 15.8; DB 22; Length 5786;

FT /tag= t
 FT /number= 10
 FT intron 36685..38529
 FT /tag= u
 FT exon 38530..38672
 FT /tag= v
 FT intron /number= 11
 FT 38673..39376
 FT /tag= w
 FT exon 39377..39562
 FT /tag= x
 FT intron /number= 12
 FT 39563..40050
 FT /tag= y
 FT exon 40051..40129
 FT /tag= z
 FT intron /number= 13
 FT 40130..45672
 FT /tag= aa
 FT exon 45673..47158
 FT /tag= ab
 FT /number= 14

WO200292629-A1.

21-NOV-2002.

14-MAY-2002; 2002WO-AU00591.

14-MAY-2001; 2001AU-0004971.

(UYQU-) UNIV QUEBENS LAND TECHNOLOGY.

Clements JA;

WPI; 2003-129264/12.

P-PSDB; AAE34613.

PT New human tweety homolog 2 polypeptides and polynucleotides, useful for
 PT producing an antigen-binding molecule that is immuno-interactive with
 PT the polypeptide or as diagnostic markers for cancers
 PS Claim 10; Page 128-156; 176pp; English.

CC The invention relates to human tweety homologue 2 (TTYH2) polypeptide and
 CC polynucleotide sequence. TTYH2 is useful for producing an antigen-binding
 CC molecule that is immuno-interactive with the polypeptide. The agent is
 CC useful for manufacturing a medicament for restoring a normal level and/or
 CC functional activity of TTYH2 expression in a patient, and for treating or
 CC preventing cancer or tumour. TTYH2 sequences may also be used to provide
 CC both drug targets and regulators to promote or inhibit one or more
 CC activities, and to provide diagnostic markers for cancers. The present
 CC sequence is human TTYH2 gene.

SQ Sequence 47999 BP; 11178 A; 12727 C; 12874 G; 11209 T; 11 other;

Query Match 79.0%; Score 15.8; DB 25; Length 47999;

Best Local Similarity 89.5%; Pred. No. 2.3e+02;

Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CTGATCGCCAAAGCAGCA 19

Db 28575 CTGTCTACCAAGCAGCA 28593

RESULT 8

AAAF22305

XX AA22305 standard; DNA; 1082138 BP.

AC AA22305;

DT 20-MAR-2001 (first entry)

XX

DE Arabidopsis thaliana chromosome 4 centromere.

XX Centromere; microsome; vector; ds.

XX Arabidopsis thaliana.

OS WO200055325-A2.

XX 21-SEP-2000.

XX 17-MAR-2000; 2000WO-US07392.

XX 18-MAR-1999; 99US-0125219.

XX 01-APR-1999; 99US-0127409.

XX 18-MAY-1999; 99US-0134770.

XX 13-SEP-1999; 99US-0153584.

XX 17-SEP-1999; 99US-0154603.

XX (UYCH-) UNIV CHICAGO.

XX Preuss D, Copenhaver G, Keith K;

XX WPI; 2000-587529/55.

XX Claim 68; Page 977-1388; 1449pp; English.

CC The present invention relates to a recombinant DNA construct of a plant
 CC (Arabidopsis thaliana) centromere. The constructs are useful for
 CC producing stably inherited microsome which can serve as vectors for
 CC the construction of transgenic plant and animal cells expressing
 CC selected proteins such as hormones, enzymes, interleukins, clotting
 CC factors, cytokines, antibodies, and growth factors.

SQ Sequence 1082138 BP; 348775 A; 194404 C; 195515 G; 343444 T; 0 other;

Query Match 79.0%; Score 15.8; DB 21; Length 1082138;

Best Local Similarity 89.5%; Pred. No. 2.8e+02;

Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 TGATCGCCAAAGCAGCAAC 20

Db 734777 TGTTGCCAAGCAGCAAC 734795

RESULT 9

ABN68569/c

XX ABN68569 standard; DNA; 543 BP.

XX 01-JUL-2002 (first entry)

XX Streptococcus polynucleotide SEQ ID NO 5051.

XX Streptococcus; GAS; GBS; group B streptococcus; Streptococcus agalactiae;

XX anti-inflammatory; infection; vaccine; meningitis; gene therapy; ds.

XX Streptococcus pyogenes.

XX WO200234771-A2.

XX 02-MAY-2002.

XX 29-OCT-2001; 2001WO-GB04789.

XX 27-OCT-2000; 2000GB-0026333.

XX 24-NOV-2000; 2000GB-0028727.

XX 07-MAR-2001; 2001GB-0005640.

XX (CHIR-) CHIRON SPA.
 PA (GENO-) INST GENOMIC RES.
 XX
 XX Telford J, Maignant V, Margarit Ros YI, Grandi G, Fraser C;
 PI Tettein H;
 DR WPI, 2002-352536/38.
 DR P-PSDB; ABP27938.
 XX
 PT New Streptococcus protein for the treatment or prevention of infection
 PT or disease caused by Streptococcus bacteria, such as meningitis, and
 PT for detecting a compound that binds to the protein -
 PS
 XX Claim 7, Page 3667; 4525pp; English.
 CC The invention relates to a protein (ABP25413-ABP30895) from group B
 CC Streptococcus/GBS (Streptococcus agalactiae) or group A streptococcus/GAS
 CC (Streptococcus pyogenes), comprising one of 5483 sequences (S1), given in
 CC the specification. The proteins have antibacterial and anti-inflammatory
 CC activity. (I), nucleic acids encoding (I), ABN6044-ABN71526 and
 CC antibodies that bind (I) are used in the manufacture of medicaments for
 CC the treatment or prevention of infection or disease caused by
 CC Streptococcus bacteria, particularly S. agalactiae and S. pyogenes.
 CC Nucleic acids encoding (I) are used to determine whether a compound binds to
 CC (I). A composition comprising (I) or a nucleic acid encoding (I), may be
 CC used as a vaccine or diagnostic composition. The disease caused by
 CC Streptococcus that is prevented or treated may be meningitis. Nucleic
 CC acids encoding (I) may be used to recombinantly produce (I) and may be
 CC used in gene therapy. Antibodies to (I) are used for affinity
 CC chromatography, immunoassays, and distinguishing/identifying
 CC Streptococcus proteins.
 XX
 SQ Sequence 543 BP; 123 A; 90 C; 93 G; 237 T; 0 other;
 Query Match 77.0%; Score 15.4; DB 24; Length 543;
 Best Local Similarity 94.1%; Pred. No. 2.6e+02;
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 3 GATCGCAACGACGA 19
 Db 486 GATCACCAACGACGA 470
 RESULT 10
 AAV30458/c
 ID AAV30458 standard; DNA; 534720 BP.
 AC AAV30458;
 XX
 XX 14-OCT-1998 (first entry)
 DE Rhizobium species plasmid pNGR234a.
 XX
 XX Rhizobium species plasmid pNGR234a.
 KW Symbol(s): open reading frame; ORF; plasmid; vector; transportation;
 KW degradation; metabolism; host range; nitrogen fixation; nodulation;
 KW legume; plant; ds.
 XX
 OS Rhizobium sp.
 XX
 XX
 FH Key Location/Qualifiers
 FT CDS 417796..418671
 FT /tag= a
 FT /standard_name= "ORF K1"
 FT /product= "Oligopeptide permease"
 FT /note= "homologous to the OppC gene"
 FT 418673..419680
 FT /tag= b
 FT /standard_name= "ORF K2"
 FT /product= "Oligopeptide permease"
 FT /note= "homologous to the Oppd gene"
 FT 419677..420738
 FT CDS

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 FT /product= "Oligopeptide permease"
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 FT 422628..424031
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 /note= "homologous to the NifH gene"
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Query Match 77.0%; Score 15.4; DB 19; Length 534720;
 Best Local Similarity 94.1%; Pred. No. 4.3e+02;
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 TGATGCCCAACGACCA 18
 Db 433213 TGATGCCCAACGACCA 433197

RESULT 11
 AAV30459/C
 ID AAV30459 standard; DNA; 536165 BP.
 AC AAV30459;
 XX
 DT 06-JUL-1999 (first entry)
 DE Rhizobium species symbiotic plasmid pNGR234.
 XX
 KW Symbiosis; open reading frame; ORF; plasmid; vector; transportation;
 degradation; metabolism; host range; nitrogen fixation; nodulation;
 legume; plant; db.
 OS Rhizobium sp.
 XX
 PN W09602560-A2.
 XX
 PD 22-JAN-1998.
 XX
 PF 10-JUL-1997; 97WO-IB00950.
 XX
 PR 20-MAY-1997; 97GB-0010395.
 XX
 PR 12-JUL-1996; 96EP-0730001.
 XX
 PA (MOLE-) INST MOLECULAR BIOTECHNOLOGY.
 XX
 PI (BIOL-) LAB BIOLOGIE MOLECULAIRE PLANTES SUPERIE.
 XX
 DR Broughton WJ, Freiberg CB, Perret XP, Rosenthal A;
 XX
 WP; 1998-110606/10.
 XX
 PT New isolated symbiotic plasmid from Rhizobium sp. NGR234 - used to
 develop products for modifying plant characteristics, e.g. nitrogen
 fixation, synthesis of compounds and stress response

PS Claim 1; Fig 3; 228bp; English.

CC This is the nucleotide sequence of the plasmid pNGR234a isolated from
XX Rhizobium sp. NGR234. Open reading frames (ORF) derivable from the
CC nucleotide sequence are claimed. The nucleotide sequences or ORFs can
CC be used e.g. in the transportation of compounds to and from an organism
CC which is a host to at least one of the nucleotide sequences, ORFs or
CC proteins, the degradation and/or metabolism of organic, inorganic,
CC natural or xenobiotic substances in a host organism or the modification
CC of the host range, nitrogen fixation abilities; for obtaining a synthetic
CC minimal set of ORFs required for functional Rhizobium-legume symbiosis,
XX especially for nodulation efficiency on host plants.
SO Sequence 536165 BP; 111291 A; 155755 C; 157864 G; 111255 T; 0 other;

Oy Query Match 77.0%; Score 15.4; DB 19; Length 536165;
Best Local Similarity 94.1%; Pred. NO. 4.3e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0

Db 433213 TGATCGCCAACGAGACA 18
||| |||
TGATCGCCAACGAGACA 433197

R**E**sult 12

A**B**GQ1593 ID ABG91593 standard; DNA; 144 BP.

XX ABQ91593;
XX
XX 01-OCT-2002 (first entry)
DT
De M. capsulatus gene #1578 for DNA array.
KM
XX Micro array; gene; de; differential expression; gene expression.
OS Methyloccoccus capsulatus.
XX WO200255655-A2.
NN
XX 18-JUL-2002.
PD
PF 14-JAN-2002; 2002WO-NO00019.
XX
XX 12-JAN-2001; 2001NO-0000235.
PR
XX 12-JAN-2001; 2001NO-0000239.
XX
PA (UNIF-) UNIFOB STITTELSSEN UNIV BERGEN.
PA (TIGR-) TIGR.
XX
PI Birkeland NK, Eidhammer I, Jonassen I, Jensen HB, Lien T;
PI Lillehaug JR, Lossius I, Eisen JA, Fraser CM, Durkin AS;
PI Salzberg SL;
XX WPI; 2002-557818/59.
DR

Novel DNA array useful for determining differential expression of
PT Methyloccoccus capsulatus genes, comprises polynucleotides or
PT oligonucleotides representative for a selective number of Methyloccoccus
PT capsulatus genes -
XX
XX Claim 14; Page 604; 678bp; English.

The invention relates to a novel DNA array giving a representation of a
CC number of Methyloccoccus capsulatus genes. The method of the invention is
CC useful for determination of the differential expression of the genes of
CC M. capsulatus, and for studying gene expression on a genomic scale and in
CC gene expression assays of M. capsulatus genes. The sequences shown in
CC ABG90016-ABG91855 represent M. capsulatus genes for use in arrays of the
invention.

Sequence 144 BP; 30 A; 50 C; 33 G; 31 T; 0 other;

QY	1	CTGATCGCCAAACGAGCAAC	20
Db	97	CTGATCGCCCATACGGCGCAC	116
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ID	ABQ91594/c	standard; DNA; 309 BP.	
XX	ABQ91594;		
AC			
XX	ABQ91594;		
DT	01-OCT-2002	(first entry)	
XX			
DE	M. capsulatus gene #1579	for DNA array.	
XX			
KW	Micro array; gene; ds; differential expression; gene expression.		
OS	Methylcococcus capsulatus.		
XX			
PN	WO200255655-A2.		
PD			
XX	18-JUL-2002.		
PF	14-JAN-2002; 2002WO-N000019.		
XX			
PR	12-JAN-2001; 2001NO-0000235.		
XX			
PR	12-JAN-2001; 2001NO-0000239.		
XX			
PA	(UNIF-) UNIFOB STITTELSEN UNIV BERGEN.		
EA	(TIGR-) TIGR.		
PI	Birkeland NK, Eidhammer I, Jonassen I, Jensen HB, Lien T,		
PI	Lillehaug JR, Lossius I, Eidsen JA, Fraser CM, Durkin AS,		
PI	Satzberg SL;		
XX			
DR	WPI: 2002-557818/59.		
XX			
PT	Novel DNA array useful for determining differential expression of		
PT	Methylcococcus capsulatus genes, comprises polynucleotides or		
PT	oligonucleotides representative for a selective number of Methylcococcus		
PT	capsulatus genes _		
XX			
XX	Claim 14; Page 604; 678bp; English.		
PS			
XX	The invention relates to a novel DNA array giving a representation of a		
CC	number of Methylcococcus capsulatus genes. The method of the invention is		
CC	useful for determination of the differential expression of the genes of		
CC	M. capsulatus, and for studying gene expression on a genomic scale and in		
CC	gene expression assays of M. capsulatus genes. The sequences shown in		
CC	ABQ90016-ABQ91855 represent M. capsulatus genes for use in arrays of the		
CC	invention.		
XX			
XX			
SQ	Sequence 309 BP; 51 A; 86 C; 109 G; 63 T; 0 other:		
Query Match	76.0%;	Score 15.2;	DB 24; Length 309;
Best Local Similarity	85.0%;	Pred. No. 3.1e+02;	
Matches 17; Conservative	0;	Mismatches 3;	Indels 0; Gaps 0;
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Db	125	CTGATCGCCATACGGCGCAC	106
RESULT 14			
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XX	ABQ65658;		
XC			

Sun Feb 15 07:29:44 2004

us-09-692-077d-15.rng

Db 182 CTCATCGCCAGACGACAC 163

RESULT 15

ABT18455

ID ABT18455 standard; DNA; 1281 BP.

XX AC ABT18455;

XX DT 16-APR-2003 (first entry)

XX DE Aspergillus fumigatus essential gene #913.

XX DE Fungicide; cytostatic; essential gene; Aspergillus fumigatus; infection;

XX DE cancer; contamination; biofilm; antibody; immune response; ds.

XX DE Aspergillus fumigatus.

XX OS WO200286090-A2.

XX PN 31-OCT-2002.

XX PD 23-APR-2002; 2002WO-US13142.

XX PE 23-APR-2001; 2001US-285697P.

XX PR 27-APR-2001; 2001US-287066P.

XX PR 05-JUN-2001; 2001US-295890P.

XX PR 09-JUL-2001; 2001US-303899P.

XX PR 31-AUG-2001; 2001US-316362P.

XX PA (ELIT-) ELITRA PHARM INC.

XX PI Jiang B, Tishkoff D, Zamudio C, Eroshkin AM, Hu W, Lemieux SM,

XX PT WPI: 2003-093124/08.

XX DR New purified or isolated nucleic acids of essential genes of

XX PT Aspergillus fumigatus, useful for treating or preventing infections by

XX PT A. fumigatus, or for treating a non-infectious disease in a subject

XX PT e.g. cancer

XX PT Disclosure; page -; 175pp; English.

XX CC The invention relates to novel purified or isolated nucleic acids of

XX CC essential genes of Aspergillus fumigatus. The isolated nucleic acids of

XX CC the invention are used to treat or prevent infections by a pathogenic

XX CC organism such as A. fumigatus, to treat a non-infectious disease in a

XX CC subject (e.g. cancer), to prevent or inhibit formation on a surface of a

XX CC biofilm comprising A. fumigatus. The polynucleotides are useful for

XX CC expressing recombinant protein for characterization, screening or

XX CC therapeutic use, as markers for host tissues in which the pathogenic

XX CC organisms invade or reside, for comparing with the DNA sequence of A.

XX CC similar biochemical activity and/or function, for comparing with DNA

XX CC sequences of other related or distant pathogenic organisms to identify

XX CC potential orthologous essential or virulence genes, for selecting and

XX CC making oligomers for attachment to a nucleic acid array for examination

XX CC of expression patterns, for raising anti-protein antibodies, as an

XX CC antigen to raise anti-DNA antibodies or to elicit another immune

XX CC response, and for identifying polynucleotides encoding the binding

XX CC with which binding occurs or to identify inhibitors of the binding

XX CC elicit immune response, as a reagent in assays designed to quantitatively

XX CC determine levels of the protein in biological fluids, as a marker for

XX CC host tissues in which pathogenic organisms invade or reside, and to

XX CC isolate correlative receptors or ligands in the case of virulence

XX CC factors. This polynucleotide sequence represents one of the essential

XX CC genes of Aspergillus fumigatus of the invention.

XX CC Sequence 1281 BP; 300 A; 358 C; 333 G; 290 T; 0 other;

Query Match 76.0%; Score 15.2; DB 25; Length 1281;

XX DT 21-AUG-2002 (first entry)

XX DE Arabidopsis thaliana polynucleotide SEQ ID NO 235.

XX DE Arabidopsis thaliana; thale cress; plant; transgenic; GMO; disease;

XX DE stress; metabolic pathway; biosynthetic pathway; nutrition; fungicide;

XX DE insecticide; antibiotic; ds.

XX OS Arabidopsis thaliana.

XX PN US2002059663-A1.

XX PD 16-MAY-2002.

XX PE 26-JAN-2001; 2001US-0770149.

XX PR 27-JAN-2000; 2000US-178506P.

XX PA (GORL/) GORLACH J.

XX PA (HAWY/) AN Y.

XX PA (HAMT/) HAMILTON C M.

XX PA (PRIC/) PRICE J L.

XX PA (RAIN/) RAINES T M.

XX PA (YUYV/) YU Y.

XX PA (RAME/) RAMEKA J G.

XX PA (PAGE/) PAGE A.

XX PA (MATH/) MATHEN A V.

XX PA (LEDF/) LEDFORD B L.

XX PA (WOES/) MOESSNER J P.

XX PA (HANS/) HANS W D.

XX PA (GARC/) GARCIA C A.

XX PA (KRIC/) KRICKER M.

XX PA (SLAT/) SLATER T.

XX PA (DAVI/) DAVIS K R.

XX PA (ALLE/) ALLEN K.

XX PA (HOFE/) HOFFMAN N.

XX PA (HURB/) HURBAN P.

XX PI Gorlach J, An Y, Hamilton CM, Price JL, Raines TM, Yu Y;

XX PI Rameka JG, Kricker M, Slater T, Davis KR, Allen K, Hoffman N;

XX PI Garcia CA, Kricker M, Slater T, Davis KR, Hoffman N;

XX PI Hurban P;

XX DR WPI: 2002-479224/51.

XX PT New nucleic acid that hybridizes to Arabidopsis thaliana sequences,

XX PT useful e.g. for preparing transgenic plants with increased resistance

XX PT or altered metabolism

XX PS Claim 1; SEQ ID NO 235; 40bp + Sequence listing; English.

XX CC The invention relates to nucleic acids (I) that hybridise under stringent

XX CC conditions to any of 999 sequences (AB065424-AB066422) or their

XX CC fragments. (I) are used to express the corresponding polypeptides (II) or

XX CC to produce genetically modified plant cells or transgenic plants, which

XX CC may have improved resistance to disease or stress, or altered

XX CC metabolic/biosynthetic pathways (for production of commercial,

XX CC nutritional or medicinal products), or generally any trait of interest,

XX CC or can be used to screen for biologically active agents (e.g. fungicides,

XX CC insecticides and antibiotics).

XX CC Note: The sequence data for this patent did not form part of the printed

XX CC specification, but was obtained in electronic format directly from the

XX CC USPTO at seqdata.uspto.gov/sequence.html?DocID=999909770149.

XX CC Sequence 705 BP; 183 A; 135 C; 183 G; 200 T; 4 other;

XX CC Query Match 76.0%; Score 15.2; DB 24; Length 705;

XX CC Best Local Similarity 85.0%; Pred. No. 3.4e+02; Indels 0; Gaps 0;

XX CC Matches 17; Conservative 0; Mismatches 3;

XX CC 1 CTCATCGCCAGACGACAC 20

Best Local Similarity 85.0%; Pred. No. 3.5e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Db	37	CTGCTGCCCAACGCCCCAC	56

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OM nucleic - nucleic search, using sw model

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Gapop 10.0 , Gapext 1.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	15.4	77.0	1698	US-09-328-352-643	Sequence 643, App
2	15.4	77.0	3032	US-09-221-017B-347	Sequence 347, App
3	15.4	77.0	536165	US-09-214-808-1	Sequence 1, Appl
4	15.2	76.0	36470	US-08-311-731A-123	Sequence 123, App
5	15.2	76.0	1664976	US-08-916-421B-1	Sequence 25, Appl
6	14.8	74.0	543	US-07-912-900-25	Sequence 25, Appl
7	14.8	74.0	543	US-08-285-309-25	Sequence 25, Appl
8	14.8	74.0	543	US-08-502-046-25	Sequence 25, Appl
9	14.8	74.0	547	US-08-313-075A-31	Sequence 31, Appl
10	14.8	74.0	4379	US-09-107-532B-2028	Sequence 2028, Ap
11	14.8	74.0	4379	US-08-592-214A-17	Sequence 17, Appl
12	14.8	74.0	4379	US-09-149-976-17	Sequence 17, Appl
13	14.8	74.0	4403765	US-09-103-840A-2	Sequence 2, Appl
14	14.8	74.0	4411529	US-09-103-840A-1	Sequence 1, Appl
15	14.2	71.0	405	US-09-643-597-218	Sequence 218, App
16	14.2	71.0	405	US-09-480-884A-218	Sequence 218, App
17	14.2	71.0	405	US-09-542-615A-218	Sequence 218, App
18	14.2	71.0	405	US-09-606-421B-218	Sequence 218, App
19	14.2	71.0	423	US-09-040-984-60	Sequence 60, Appl
20	14.2	71.0	423	US-09-123-912-60	Sequence 60, Appl
21	14.2	71.0	423	US-09-643-597-60	Sequence 60, Appl
22	14.2	71.0	423	US-09-480-884A-60	Sequence 60, Appl
23	14.2	71.0	423	US-09-542-615A-60	Sequence 60, Appl
24	14.2	71.0	423	US-09-606-421B-60	Sequence 60, Appl
25	14.2	71.0	433	US-09-606-421B-60	Sequence 60, Appl
26	14.2	71.0	575	US-09-740-235-32	Sequence 32, Appl
27	14.2	71.0	814	US-09-669-751-108	Sequence 108, Appl
				US-09-020-956-36	Sequence 36, Appl

28	14.2	71.0	814	US-09-030-607-36	Sequence 36, Appl
29	14.2	71.0	814	US-09-439-313-36	Sequence 36, Appl
30	14.2	71.0	814	US-09-352-616A-36	Sequence 36, Appl
31	14.2	71.0	814	US-09-232-149A-36	Sequence 36, Appl
32	14.2	71.0	896	US-09-221-017B-199	Sequence 199, App
33	14.2	71.0	1185	US-09-252-991A-1931	Sequence 1931, App
34	14.2	71.0	1194	US-08-989-478-13	Sequence 13, Appl
35	14.2	71.0	1194	US-08-996-685-13	Sequence 13, Appl
36	14.2	71.0	1428	US-09-328-352-1571	Sequence 1571, Ap
37	14.2	71.0	1449	US-09-107-532A-858	Sequence 858, App
38	14.2	71.0	1597	US-08-989-478-9	Sequence 9, Appl
39	14.2	71.0	1597	US-08-996-685-9	Sequence 9, Appl
40	14.2	71.0	1608	US-08-989-478-11	Sequence 11, Appl
41	14.2	71.0	1608	US-08-996-685-11	Sequence 11, Appl
42	14.2	71.0	2011	US-08-989-478-6	Sequence 6, Appl
43	14.2	71.0	2011	US-08-989-478-7	Sequence 7, Appl
44	14.2	71.0	2011	US-08-996-685-6	Sequence 6, Appl
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ALIGNMENTS

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RESULT 1
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; Sequence 643, Application US/09328352
; Patent No. 6562958
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
; FILE REFERENCE: GTC99-03PA
; CURRENT APPLICATION NUMBER: US/09/328,352
; NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 643
; LENGTH: 1698
; TYPE: DNA
; ORGANISM: Acinetobacter baumannii
US-09-328-352-643

Query Match      77.0%; Score 15.4; DB 4; Length 1698;
Best Local Similarity 94.1%; Pred. No. 44;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      4 ATCGCCAAACGACGAC 20
DB      143 ATCGCCAAACGACGAC 127

RESULT 2
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; Sequence 347, Application US/09221017B
; Patent No. 6444799
; GENERAL INFORMATION:
; APPLICANT: Ross, Bruce C.
; TITLE OF INVENTION: P. GINGIVALIS NUCLEOTIDES AND USES THEREOF
; NUMBER OF SEQUENCES: 1120
; CORRESPONDENCE ADDRESS:
; ADDRESSER: MORRISON & FORSTER
; STREET: 755 PAGE MILL ROAD
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: Windows
; SOFTWARE: FASTSEQ for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/221,017B
; FILING DATE: 23-DEC-1998

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CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PP1182
FILING DATE: 31-DEC-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PP1546
FILING DATE: 30-JAN-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PP2911
FILING DATE: 09-APR-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/AU98/01023
FILING DATE: 10-DEC-1998
ATTORNEY/AGENT INFORMATION:
NAME: Monroy, Gladys H
REGISTRATION NUMBER: 32,430
REFERENCE/DOCKET NUMBER: 27340-20021.00
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-813-5600
TELEFAX: 650-494-0792
TELEX: 706141
INFORMATION FOR SEQ ID NO: 347:
SEQUENCE CHARACTERISTICS:
LENGTH: 3032 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: UNKNOWN
ORIGINAL SOURCE:
ORGANISM: PORPHYROMONAS GINGIVALIS
FEATURE:
NAME/KEY: misc feature
LOCATION: 1...3032
US-09-221-017B-347

Query Match 77.0%; Score 15.4; DB 4; Length 3032;
Best Local Similarity 94.1%; Pred. No. 47;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CTGATGCCCAAGAGC 17
Db 2855 CTGATGCCCATCGAGC 2871

RESULT 3
US-09-214-808-1/c
Sequence 1, Application US/09214808A
Patent No. 6475793
GENERAL INFORMATION:
APPLICANT: Rosenthal, Andre
APPLICANT: Freiberg, Christoph
APPLICANT: Perret, Xavier Philippe
APPLICANT: Broughton, William John
TITLE OF INVENTION: Genomic Sequence of Rhizobium SP. NGR 234 Symbiotic
Patent No. 6475793
TITLE OF INVENTION: Plasmid
FILE REFERENCE: CARP0068
CURRENT APPLICATION NUMBER: US/09/214,808A
CURRENT FILING DATE: 1999-06-22
PRIOR APPLICATION NUMBER: PCT/IB97/00950
PRIOR FILING DATE: 1997-07-10
NUMBER OF SEQ ID NOS: 1
SOFTWARE: Patentin Ver. 2.6.1
SEQ ID NO 1
LENGTH: 536165
TYPE: DNA
ORGANISM: Rhizobium
US-09-214-808-1

Query Match 77.0%; Score 15.4; DB 4; Length 536165;
Best Local Similarity 94.1%; Pred. No. 80;

Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 TGATGCCCAAGAGCA 18
Db 433213 TGATGCCCAATCGAGCA 433197

RESULT 4
US-08-311-731A-123
Sequence 123, Application US/08311731A
Patent No. 6583266
GENERAL INFORMATION:
APPLICANT: SMITH, DOUGLAS
APPLICANT: MAO, JEN-I
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES
TITLE OF INVENTION: RELATING TO MYCOBACTERIUM TUBERCULOSIS AND LAPRAE FOR
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
NUMBER OF SEQUENCES: 411
CORRESPONDENCE ADDRESSES:
ADDRESSER: WOLF, GREENFIELD & SACKS, P.C.
STREET: 600 ATLANTIC AVENUE
CITY: BOSTON
STATE: MASSACHUSETTS
COUNTRY: USA
ZIP: 02210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/311,731A
FILING DATE:
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: GATES, EDWARD R.
REGISTRATION NUMBER: 31,616
REFERENCE/DOCKET NUMBER: C0044/7125
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/720-3500
TELEFAX: 617/720-2441
INFORMATION FOR SEQ ID NO: 123:
SEQUENCE CHARACTERISTICS:
LENGTH: 36470 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: MYCOBACTERIUM LEPRAE
US-08-311-731A-123

Query Match 76.0%; Score 15.2; DB 4; Length 36470;
Best Local Similarity 85.0%; Pred. No. 79;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CTGATGCCCAAGAGCAAC 20
Db 3894 CTAAATGCCCAACAGCAAC 3913

RESULT 5
US-08-916-421B-1/c
Sequence 1, Application US/08916421B
Patent No. 6503729
GENERAL INFORMATION:
APPLICANT: Built et al.
TITLE OF INVENTION: Complete Genome Sequence of the Methanogenic Archaeon, Methanococcus
Patent No. 6503729
TITLE OF INVENTION: Janaschii
FILE REFERENCE: PB275


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CURRENT APPLICATION NUMBER: US/08/916,421B
CURRENT FILING DATE: 1997-08-22
PRIOR APPLICATION NUMBER: US 60/024,428
PRIOR FILING DATE: 1996-08-22
NUMBER OF SEQ ID NOS: 3
SOFTWARE: PatentIn version 3.1
SEQ ID NO 1
LENGTH: 1664976
TYPE: DNA
ORGANISM: Methanococcus jamaeschi
FEATURE:
NAME/KEY: misc_feature
LOCATION: (28222)..(28222)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc_feature
LOCATION: (28257)..(28258)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc_feature
LOCATION: (84773)..(84773)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc_feature
LOCATION: (84808)..(84808)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc_feature
LOCATION: (84812)..(84812)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc_feature
LOCATION: (98159)..(98159)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc_feature
LOCATION: (98170)..(98170)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc_feature
LOCATION: (98239)..(98239)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc_feature
LOCATION: (98266)..(98266)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc_feature
LOCATION: (98343)..(98343)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc_feature
LOCATION: (103998)..(103998)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc_feature
LOCATION: (148948)..(148948)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc_feature
LOCATION: (163385)..(163385)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc_feature
LOCATION: (191989)..(191989)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc_feature
LOCATION: (191995)..(191995)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc_feature
LOCATION: (231980)..(231980)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc_feature
LOCATION: (234187)..(234187)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc_feature
LOCATION: (234220)..(234220)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc_feature
LOCATION: (234814)..(234814)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc_feature
LOCATION: (309398)..(309398)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc_feature
LOCATION: (309418)..(309418)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc_feature
LOCATION: (312837)..(312837)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc_feature
LOCATION: (312993)..(312993)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc_feature
LOCATION: (319226)..(319226)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc_feature
LOCATION: (559167)..(559167)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc_feature
LOCATION: (559241)..(559241)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc_feature
LOCATION: (600992)..(600992)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc_feature
LOCATION: (622708)..(622708)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc_feature
LOCATION: (657081)..(657081)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc_feature
LOCATION: (657203)..(657203)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc_feature
LOCATION: (674435)..(674435)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc_feature
LOCATION: (682442)..(682442)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc_feature
LOCATION: (713652)..(713652)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc_feature
LOCATION: (741684)..(741684)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc_feature
LOCATION: (779455)..(779455)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc_feature
LOCATION: (779676)..(779676)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc_feature
LOCATION: (855539)..(855539)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc_feature
LOCATION: (871619)..(871619)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc_feature
LOCATION: (1084830)..(1084830)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc_feature
LOCATION: (1096846)..(1096846)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc_feature
LOCATION: (1119881)..(1119881)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc_feature
LOCATION: (1310988)..(1310988)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc_feature
LOCATION: (1333224)..(1333224)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc_feature
LOCATION: (1349473)..(1349473)
OTHER INFORMATION: n equals a, t, c, or g

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NAME/KEY: misc feature
LOCATION: (1349491)...(1349491)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc feature
LOCATION: (1470091)...(1470091)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc feature
LOCATION: (1569020)...(1569020)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc feature
LOCATION: (1602912)...(1602912)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc feature
LOCATION: (1603734)...(1603734)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc feature
LOCATION: (1637998)...(1637998)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc feature
LOCATION: (1664854)...(1664854)
OTHER INFORMATION: n equals a, t, c, or g
US-08-916-421B-1

Query Match 76.0%; Score 15.2; DB 4; Length 1664976;
Best Local Similarity 85.0%; Pred. No. 97;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CTGATCGCCAAACGAGCAAC 20
DB 1565938 CTTATAGCCAAACGAGCAAC 1565919

RESULT 6
US-07-912-900-25
Sequence 25, Application US/07912900
Patent No. 5349125
GENERAL INFORMATION:
APPLICANT: Holton, Timothy A.
APPLICANT: Cornish, Edwin C.
APPLICANT: Kovacic, Filipa
APPLICANT: Tanaka, Yoshikazu
APPLICANT: Lester, Diane R.
TITLE OF INVENTION: GENETIC SEQUENCES ENCODING FLAVONOID
TITLE OF INVENTION: PATHWAY ENZYMES AND USES THEREFOR
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: Scully, Scott, Murphy & Presser
STREET: 400 Garden City Plaza
CITY: Garden City
STATE: New York
COUNTRY: U.S.A.
ZIP: 11530
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/912,900
FILING DATE: 19920713
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Digilio, Frank S.
REGISTRATION NUMBER: 31,346
REFERENCE/DOCKET NUMBER: 8633
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 742-4343
TELEFAX: (516) 742-4366
TELEX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 543 base pairs
TYPE: NUCLEIC ACID

STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-07-912-900-25

Query Match 74.0%; Score 14.8; DB 1; Length 543;
Best Local Similarity 88.9%; Pred. No. 80;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 TGATGCCAAACGAGCAA 19
DB 69 TGATGCCAAACTATCAA 86

RESULT 7
US-08-285-309-25
Sequence 25, Application US/08285309
Patent No. 5569832
GENERAL INFORMATION:
APPLICANT: Holton, Timothy A.
APPLICANT: Cornish, Edwin C.
APPLICANT: Kovacic, Filipa
APPLICANT: Tanaka, Yoshikazu
APPLICANT: Lester, Diane R.
TITLE OF INVENTION: GENETIC SEQUENCES ENCODING A 3,5'-
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: Scully, Scott, Murphy & Presser
STREET: 400 Garden City Plaza
CITY: Garden City
STATE: New York
COUNTRY: U.S.A.
ZIP: 11530
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/285,309
FILING DATE: 03-AUG-1994
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Digilio, Frank S.
REGISTRATION NUMBER: 31,346
REFERENCE/DOCKET NUMBER: 8633Z
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 742-4343
TELEFAX: (516) 742-4366
TELEX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 543 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-285-309-25

Query Match 74.0%; Score 14.8; DB 1; Length 543;
Best Local Similarity 88.9%; Pred. No. 80;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 TGATGCCAAACGAGCAA 19
DB 69 TGATGCCAAACTATCAA 86

RESULT 8
US-08-502-046-25
Sequence 25, Application US/08502046
Patent No. 5861487

GENERAL INFORMATION:
APPLICANT: Holton, Timothy A.
APPLICANT: Cornish, Edwina C.
APPLICANT: Kovacic, Filipa
APPLICANT: Tanaka, Yoshikazu
APPLICANT: Lester, Diane R.
TITLE OF INVENTION: GENETIC SEQUENCES ENCODING A 3,5'-
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Scully, Scott, Murphy & Presser
STREET: 400 Garden City Plaza
CITY: Garden City
STATE: New York
COUNTRY: U.S.A.
ZIP: 11530
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/502,046
FILING DATE: 14-JUL-1995
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/285,309
FILING DATE: 03-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: Digilio, Frank S.
REGISTRATION NUMBER: 31,346
REFERENCE/DOCKET NUMBER: 86332
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 742-4343
TELEFAX: (516) 742-4366
TELEX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 543 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-502-046-25

Query Match 74.0%; Score 14.8; DB 2; Length 543;
Best Local Similarity 88.9%; Pred. No. 80;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 TGATGCCCAAGAGCAA 19
DB 69 TGATGCCCAACTATCAA 86

RESULT 9
US-08-313-075A-31
Sequence 31, Application US/08313075A
Patent No. 5639870
GENERAL INFORMATION:
APPLICANT: Holton, Timothy A.
APPLICANT: Cornish, Edwina C.
APPLICANT: Tanaka, Yoshikazu
TITLE OF INVENTION: GENETIC SEQUENCES ENCODING FLAVONOID
NUMBER OF SEQUENCES: 58
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Scully, Scott, Murphy & Presser
STREET: 400 Garden City Plaza
CITY: Garden City
STATE: New York
COUNTRY: U.S.A.
ZIP: 11530
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/313,075A
FILING DATE: 30-NOV-1994
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: AU PL 1538/92
FILING DATE: 27-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: AU PL 6698/93
FILING DATE: 07-JAN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: AU PCT/AU93/00127
FILING DATE: 25-MAR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Digilio, Frank S.
REGISTRATION NUMBER: 31,346
REFERENCE/DOCKET NUMBER: 9433
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 742-4343
TELEFAX: (516) 742-4366
TELEX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
LENGTH: 547 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..514
US-08-313-075A-31

Query Match 74.0%; Score 14.8; DB 1; Length 547;
Best Local Similarity 88.9%; Pred. No. 80;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 TGATGCCCAAGAGCAA 19
DB 69 TGATGCCCAACTATCAA 86

RESULT 10
US-09-107-532A-2028/c
Sequence 2028, Application US/09107532A
Patent No. 6583275
GENERAL INFORMATION:
APPLICANT: Lynn A Doucette-Stamm and David Bush
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
NUMBER OF SEQUENCES: 7310
CORRESPONDENCE ADDRESSES:
ADDRESSEE: GENOME THERAPEUTICS CORPORATION
STREET: 100 Beaver Street
CITY: Waltham
STATE: Massachusetts
COUNTRY: USA
ZIP: 02354
COMPUTER READABLE FORM:
MEDIUM TYPE: CD-ROM ISO9660
COMPUTER: PC
OPERATING SYSTEM: <Unknown>
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107,532A
FILING DATE: 30-Jun-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998

APPLICATION NUMBER: 60/051571
FILING DATE: July 2, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Arinello, Pamela Deneka
REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-012
TELECOMMUNICATION INFORMATION:
TELEPHONE: (781) 893-5007
TELEFAX: (781) 893-8277
INFORMATION FOR SEQ ID NO: 2028:
SEQUENCE CHARACTERISTICS:
LENGTH: 810 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Enterococcus faecium
FEATURE:
NAME/KEY: misc feature
LOCATION: (B) LOCATION 1... 810
SEQUENCE DESCRIPTION: SEQ ID NO: 2028:
US-09-107-532A-2028
Query Match 74.0%; Score 14.8; DB 4; Length 810;
Best Local Similarity 88.9%; Pred. No. 84;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 2 TGATGCCCAACGACGAA 19
DB 628 TGATGCCCAACGACGAA 611
RESULT 11
US-08-592-214A-17
Sequence 17, Application US/08592214A
Patent No. 5811536
GENERAL INFORMATION:
APPLICANT: Yanofsky, Martin F.
TITLE OF INVENTION: Cauliflower Floral Meristem Identity
TITLE OF INVENTION: Genes and Methods of Using Same
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell and Flores
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: United States
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/592,214A
FILING DATE: 26-JAN-1996
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-UD 1927
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 4379 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear

FEATURE:
NAME/KEY: unsure
LOCATION: 2095..2098
OTHER INFORMATION: /note= "N" = one or more
OTHER INFORMATION: nucleotides."
FEATURE:
NAME/KEY: misc feature
LOCATION: 1..4379
OTHER INFORMATION: /note= "sequence = Arabidopsis
OTHER INFORMATION: thaliana APl gene"
US-08-592-214A-17
Query Match 74.0%; Score 14.8; DB 1; Length 4379;
Best Local Similarity 88.9%; Pred. No. 1e+02; 2; Indels 0; Gaps 0;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 2 TGATGCCCAACGACGAA 19
DB 3961 TGATGCCCAACGACGAA 3978
RESULT 12
US-09-149-976-17
Sequence 17, Application US/09149976
Patent No. 6127123
GENERAL INFORMATION:
APPLICANT: Yanofsky, Martin F.
TITLE OF INVENTION: Cauliflower Floral Meristem Identity
TITLE OF INVENTION: Genes and Methods of Using Same
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell & Flores LLP
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: United States
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/149,976
FILING DATE: 09-SEP-1998
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/592,214
FILING DATE: 26-JAN-1996
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-UD 3291
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 4379 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
FEATURE:
NAME/KEY: unsure
LOCATION: 2095..2098
OTHER INFORMATION: /note= "N" = one or more
OTHER INFORMATION: nucleotides."
FEATURE:
NAME/KEY: misc feature
LOCATION: 1..4379
OTHER INFORMATION: /note= "sequence = Arabidopsis
OTHER INFORMATION: thaliana APl gene"
US-09-149-976-17

Query Match 74.0%; Score 14.8; DB 3; Length 4379;
Best Local Similarity 88.9%; Pred. No. 1e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 TGATGCCCAACGAGCA 19
Db 3961 TGATGCCCAACGAGCA 3978

RESULT 13

US-09-103-840A-2
; Sequence 2, Application US/09103840A
; Patent No. 6294328
; GENERAL INFORMATION:
; APPLICANT: FLEISCHMAN, Robert D.
; APPLICANT: WHITE, Owen R.
; APPLICANT: FRASER, Claire M.
; APPLICANT: VENTER, John C.
; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
; FILE REFERENCE: 24366-20007.00
; CURRENT APPLICATION NUMBER: US/09/103,840A
; CURRENT FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 2
; LENGTH: 4403765
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; FEATURE:
; OTHER INFORMATION: CDC 1551
; OTHER INFORMATION: "n" bases at various positions throughout the sequence
US-09-103-840A-2

Query Match 74.0%; Score 14.8; DB 3; Length 4403765;
Best Local Similarity 88.9%; Pred. No. 89;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 GATGCCCAACGAGCAAC 20
Db 682842 GATGCCCAACGAGCAAC 682859

RESULT 14

US-09-103-840A-1
; Sequence 1, Application US/09103840A
; Patent No. 6294328
; GENERAL INFORMATION:
; APPLICANT: FLEISCHMAN, Robert D.
; APPLICANT: WHITE, Owen R.
; APPLICANT: FRASER, Claire M.
; APPLICANT: VENTER, John C.
; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
; FILE REFERENCE: 24366-20007.00
; CURRENT APPLICATION NUMBER: US/09/103,840A
; CURRENT FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 1
; LENGTH: 4411529
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; OTHER INFORMATION: H37Rv
US-09-103-840A-1

Query Match 74.0%; Score 14.8; DB 3; Length 4411529;
Best Local Similarity 88.9%; Pred. No. 89;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 3 GATGCCCAACGAGCAAC 20

Db 681399 GATGCCCAACGAGCAAC 681416

RESULT 15

US-09-643-597-218
; Sequence 218, Application US/09643597
; Patent No. 6426072
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongrong
; APPLICANT: Fan, Liqun
; APPLICANT: Kalos, Michael D.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Hosken, Nancy
; APPLICANT: Fanger, Gary R.
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Henderson, Robert A.
; APPLICANT: McNeill, Patricia D.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.455C11
; CURRENT APPLICATION NUMBER: US/09/643,597
; CURRENT FILING DATE: 2000-08-21
; NUMBER OF SEQ ID NOS: 369
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 218
; LENGTH: 405
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-643-597-218

Query Match 71.0%; Score 14.2; DB 4; Length 405;
Best Local Similarity 84.2%; Pred. No. 1.6e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CTGATGCCCAACGAGCA 19
Db 77 CTGATGCCCAACGAGCA 95

Search completed: February 12, 2004, 06:08:10
Job time : 48.3171 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Comphen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 12, 2004, 04:42:03 ; Search time 113.659 Seconds
(without alignments)
648.193 Million cell updates/sec

Title: US-09-692-077D-15

Perfect score: 20

Sequence: 1 CTGATGCCAAAGAGCAAC 20

Scoring table: IDENTITY NUC

Gapop 10.0, Gapext 1.0

Searched: 2449703 seqs, 1841816367 residues 4899406

Total number of hits satisfying chosen parameters:

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Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database: Published Applications NA.*

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11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq.*
12: /cgn2_6/ptodata/1/pubpna/US09C_PUB.seq.*
13: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq.*
14: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq.*
15: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq.*
16: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq.*
17: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq.*
18: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	20	100.0	20	US-10-001-073-15	Sequence 15, Appl
2	16	80.0	3325	US-10-369-493-44911	Sequence 44911, A
3	15.8	79.0	277	US-09-878-574-7065	Sequence 7065, Ap
4	15.8	79.0	1976	US-09-878-574-4681	Sequence 4681, Ap
5	15.8	79.0	5786	US-09-764-878-240	Sequence 240, App
6	15.8	79.0	5786	US-10-079-854-240	Sequence 240, App
7	15.4	77.0	536165	US-09-939-964-1	Sequence 1, Appl
8	15.2	76.0	705	US-09-770-149-235	Sequence 235, App
9	15.2	76.0	1281	US-10-128-714-1219	Sequence 1219, Ap
10	15.2	76.0	1284	US-10-128-714-2219	Sequence 2219, Ap
11	15.2	76.0	1359	US-09-938-842A-2021	Sequence 2021, Ap
12	15.2	76.0	1359	US-09-938-842A-2021	Sequence 2021, Ap
13	15.2	76.0	2031	US-10-108-605-206	Sequence 206, App
14	15.2	76.0	2193	US-09-815-242-6644	Sequence 6644, Ap
15	15.2	76.0	2241	US-10-108-605-116	Sequence 116, App

C 16	15.2	76.0	3184	14	US-10-108-605-324	Sequence 324, App
C 17	15.2	76.0	3281	15	US-10-128-714-219	Sequence 219, App
C 18	15.2	76.0	4779	9	US-09-764-878-216	Sequence 216, App
C 19	15.2	76.0	4779	15	US-10-079-854-216	Sequence 216, App
C 20	15	75.0	1449	12	US-10-369-493-32914	Sequence 32914, A
C 21	15	75.0	1449	12	US-10-369-493-32914	Sequence 33107, A
C 22	14.8	74.0	391	10	US-09-960-352-5967	Sequence 5967, App
C 23	14.8	74.0	391	10	US-09-983-965-958	Sequence 958, App
C 24	14.8	74.0	416	10	US-09-983-965-623	Sequence 623, App
C 25	14.8	74.0	987	12	US-10-369-493-28292	Sequence 28292, A
C 26	14.8	74.0	993	12	US-10-369-493-31049	Sequence 31049, A
C 27	14.8	74.0	1392	15	US-10-036-959B-2	Sequence 2, Appl
C 28	14.8	74.0	1527	15	US-10-156-761-350	Sequence 350, App
C 29	14.8	74.0	1741	15	US-10-142-835-29	Sequence 29, Appl
C 30	14.8	74.0	1795	12	US-10-369-493-36531	Sequence 36531, A
C 31	14.8	74.0	2091	12	US-10-108-260A-936	Sequence 936, App
C 32	14.8	74.0	2337	12	US-10-369-493-45576	Sequence 45576, A
C 33	14.8	74.0	2592	10	US-09-938-842A-1537	Sequence 1537, App
C 34	14.8	74.0	2592	12	US-09-938-842A-1537	Sequence 1537, App
C 35	14.8	74.0	3082	12	US-10-398-221-3557	Sequence 3557, App
C 36	14.8	74.0	5848	15	US-10-128-714-380	Sequence 380, App
C 37	14.8	74.0	5849	15	US-10-128-714-5380	Sequence 5380, App
C 38	14.8	74.0	9025608	15	US-10-156-761-1	Sequence 1, Appl
C 39	14.4	72.0	315	12	US-09-864-408A-3499	Sequence 3499, App
C 40	14.4	72.0	582	13	US-10-029-386-684	Sequence 684, App
C 41	14.4	72.0	808	14	US-10-027-632-173804	Sequence 173804, App
C 42	14.4	72.0	808	14	US-10-027-632-173804	Sequence 173804, App
C 43	14.4	72.0	1311	10	US-09-070-927A-3	Sequence 3, Appl
C 44	14.4	72.0	1455	13	US-10-138-701-60	Sequence 60, Appl
C 45	14.4	72.0	1501	12	US-10-398-221-1962	Sequence 1962, App

ALIGNMENTS

RESULT 1
US-10-001-073-15
; Sequence 15, Application US/10001073
; Publication No. US20030113725A1
; GENERAL INFORMATION:
; APPLICANT: Liggett, Stephen
; TITLE OF INVENTION: Alpha-2-adrenergic receptor polymorphisms
; FILE REFERENCE: 13073-PCT
; CURRENT APPLICATION NUMBER: US/10/001, 073
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 15
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-001-073-15

Query Match 100.0%; Score 20; DB 15; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.57;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGATGCCAAAGAGCAAC 20
DB 1 CTGATGCCAAAGAGCAAC 20

RESULT 2
US-10-369-493-44911/C
; Sequence 44911, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng

```

; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 44911
; LENGTH: 3325
; TYPE: DNA
; ORGANISM: Xenorhabdus nematophilus
; US-10-369-493-44911

Query Match      80.0%; Score 16; DB 12; Length 3325;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      5 TCGCCAAACGAGCAAC 20
Db      1189 TCGCCAAACGAGCAAC 1174

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RESULT 3
; US-09-878-574-7065/C
; Sequence 7065, Application US/09878574
; Patent No. US20020110548A1
; GENERAL INFORMATION:
; APPLICANT: Byrum, Joseph R.
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Thompson, Michael D.
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; FILE REFERENCE: 38-21(15401)B
; CURRENT APPLICATION NUMBER: US/09/878,574
; CURRENT FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: 09/333,535
; PRIOR FILING DATE: 1999-06-14
; NUMBER OF SEQ ID NOS: 15775
; SEQ ID NO 7065
; LENGTH: 277
; TYPE: DNA
; ORGANISM: Glycine max
; OTHER INFORMATION: Clone ID: 701099380H1
; US-09-878-574-7065

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Query Match      79.0%; Score 15.8; DB 10; Length 277;
Best Local Similarity 89.5%; Pred. No. 1.3e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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QY      2 TGATGCCAAACGAGCAAC 20
Db      277 TGATGCCAAACGAGCAAC 259

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RESULT 4
; US-09-878-574-4681
; Sequence 4681, Application US/09878574
; Patent No. US20020110548A1
; GENERAL INFORMATION:
; APPLICANT: Byrum, Joseph R.
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Thompson, Michael D.
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; FILE REFERENCE: 38-21(15401)B
; CURRENT APPLICATION NUMBER: US/09/878,574
; CURRENT FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: 09/333,535
; PRIOR FILING DATE: 1999-06-14
; NUMBER OF SEQ ID NOS: 15775
; SEQ ID NO 4681
; LENGTH: 1976

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; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(1976)
; OTHER INFORMATION: unsure at all n locations
; OTHER INFORMATION: Clone ID: LIB3028-039-Q1-B2-G12
; US-09-878-574-4681

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Query Match      79.0%; Score 15.8; DB 10; Length 1976;
Best Local Similarity 85.0%; Pred. No. 1.6e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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QY      1 CTGATCGCCAAACGAGCAAC 20
Db      1174 CTGATCGCCAAACGAGCAAC 1193

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RESULT 5
; US-09-764-878-240
; Sequence 240, Application US/09764878
; Patent No. US20020090615A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PA121
; CURRENT APPLICATION NUMBER: US/09/764,878
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 428
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 240
; LENGTH: 5786
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-764-878-240

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Query Match      79.0%; Score 15.8; DB 9; Length 5786;
Best Local Similarity 89.5%; Pred. No. 1.8e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```

```

QY      2 TGATGCCAAACGAGCAAC 20
Db      818 TTATGCCAAATGAGCAAC 836

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```

RESULT 6
; US-10-079-854-240
; Sequence 240, Application US/10079854
; Publication No. US20030054368A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PA121C1
; CURRENT APPLICATION NUMBER: US/10/079,854
; CURRENT FILING DATE: 2002-02-22
; Prior Application removed - See file Wrapper or Palm
; NUMBER OF SEQ ID NOS: 428
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 240
; LENGTH: 5786
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-079-854-240

```

```

Query Match      79.0%; Score 15.8; DB 15; Length 5786;
Best Local Similarity 89.5%; Pred. No. 1.8e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```

```

QY      2 TGATGCCAAACGAGCAAC 20
Db      818 TTATGCCAAATGAGCAAC 836

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RESULT 7
US-09-939-964-1/c
; Sequence 1, Application US/09939964
; Publication No. US20030054522A1
; GENERAL INFORMATION:
; APPLICANT: Rosenthal, Andre
; APPLICANT: Freiberg, Christoph
; APPLICANT: Perret, Xavier Philippe
; APPLICANT: Broughon, William John
; TITLE OF INVENTION: Genomic Sequence of Rhizobium SP. NGR 234 Symbiotic
; TITLE OF INVENTION: Plasmid
; FILE REFERENCE: CARP0068
; CURRENT APPLICATION NUMBER: US/09/939,964
; CURRENT FILING DATE: 2001-08-27
; PRIOR APPLICATION NUMBER: 09/214,808
; PRIOR FILING DATE: 1999-06-22
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 536165
; TYPE: DNA
; ORGANISM: Rhizobium
US-09-939-964-1

Query Match 77.0%; Score 15.4; DB 11; Length 536165;
Best Local Similarity 94.1%; Pred. No. 4.5e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 CTGATGCCAAGACGACA 18
Db 433213 TGATCGCAATCGACGA 433197

RESULT 8
US-09-770-149-235/c
; Sequence 235, Application US/09770149
; Patent No. US2002005963A1
; GENERAL INFORMATION:
; APPLICANT: Goriach, Jörn
; APPLICANT: An, Yong-Qiang
; APPLICANT: Hamilton, Carol M.
; APPLICANT: Price, Jennifer L.
; APPLICANT: Raines, Tracy M.
; APPLICANT: Yu, Yang
; APPLICANT: Rameaka, Joshua G.
; APPLICANT: Page, Amy
; APPLICANT: Matthew, Abraham V.
; APPLICANT: Ledford, Brooke L.
; APPLICANT: Moesener, Jeffrey P.
; APPLICANT: Haas, William David
; APPLICANT: Garcia, Carlos A.
; APPLICANT: Krickler, Maja
; APPLICANT: Slader, Ted
; APPLICANT: Davis, Keith R.
; APPLICANT: Allen, Keith
; APPLICANT: Hoffman, Neil
; APPLICANT: Hurdan, Patrick
; TITLE OF INVENTION: Expressed Sequences of Arabidopsis
; TITLE OF INVENTION: thaliana
; FILE REFERENCE: 2024 (PARA-013PRV)
; CURRENT APPLICATION NUMBER: US/09/770,149
; CURRENT FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 60/178,506
; PRIOR FILING DATE: 2000-01-27
; NUMBER OF SEQ ID NOS: 999
; SOFTWARE: PatSeq for Windows Version 4.0
; SEQ ID NO 235
; LENGTH: 705
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: misc_feature

; LOCATION: (1)...(705)
; OTHER INFORMATION: n = A,T,C or G
US-09-770-149-235

Query Match 76.0%; Score 15.2; DB 9; Length 705;
Best Local Similarity 85.0%; Pred. No. 3.1e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CTGATGCCAAGACGACAC 20
Db 182 CTGATGCCAAGACGACAC 163

RESULT 9
US-10-128-714-1219
; Sequence 1219, Application US/10128714
; Publication No. US20030119013A1
; GENERAL INFORMATION:
; APPLICANT: Jiang, Bo
; APPLICANT: Hu, Wengqi
; APPLICANT: Tishkoff, Daniel
; APPLICANT: Zamudio, Carlos
; APPLICANT: Eroshkin, Alexey M
; APPLICANT: Lemieux, Sebastien M
; TITLE OF INVENTION: Identification of Essential Genes in Aspergillus fumigatus and
; FILE REFERENCE: 10182-018-999
; CURRENT APPLICATION NUMBER: US/10/128,714
; CURRENT FILING DATE: 2002-04-23
; PRIOR APPLICATION NUMBER: US 60/285,697
; PRIOR FILING DATE: 2001-04-23
; PRIOR APPLICATION NUMBER: US 60/287,066
; PRIOR FILING DATE: 2001-04-27
; PRIOR APPLICATION NUMBER: US 60/295,890
; PRIOR FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: US 60/303,899
; PRIOR FILING DATE: 2001-07-09
; PRIOR APPLICATION NUMBER: US 60/316,362
; PRIOR FILING DATE: 2001-08-31
; NUMBER OF SEQ ID NOS: 8603
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1219
; LENGTH: 1281
; TYPE: DNA
; ORGANISM: Aspergillus fumigatus
US-10-128-714-1219

Query Match 76.0%; Score 15.2; DB 15; Length 1281;
Best Local Similarity 85.0%; Pred. No. 3.3e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CTGATGCCAAGACGACAC 20
Db 37 CTGATGCCAAGACGACAC 56

RESULT 10
US-10-128-714-2219
; Sequence 2219, Application US/10128714
; Publication No. US20030119013A1
; GENERAL INFORMATION:
; APPLICANT: Jiang, Bo
; APPLICANT: Hu, Wengqi
; APPLICANT: Tishkoff, Daniel
; APPLICANT: Zamudio, Carlos
; APPLICANT: Eroshkin, Alexey M
; APPLICANT: Lemieux, Sebastien M
; TITLE OF INVENTION: Identification of Essential Genes in Aspergillus fumigatus and
; FILE REFERENCE: 10182-018-999
; CURRENT APPLICATION NUMBER: US/10/128,714
; CURRENT FILING DATE: 2002-04-23
; PRIOR APPLICATION NUMBER: US 60/285,697

FILE FILING DATE: 2001-04-23
PRIOR APPLICATION NUMBER: US 60/287,066
PRIOR FILING DATE: 2001-04-27
PRIOR APPLICATION NUMBER: US 60/295,890
PRIOR FILING DATE: 2001-06-05
PRIOR APPLICATION NUMBER: US 60/303,899
PRIOR FILING DATE: 2001-07-09
PRIOR APPLICATION NUMBER: US 60/316,362
PRIOR FILING DATE: 2001-08-31
NUMBER OF SEQ ID NOS: 8603
SOFTWARE: PatentIn version 3.1
SEQ ID NO 2219
LENGTH: 1284
TYPE: DNA
ORGANISM: Aspergillus fumigatus
US-10-128-714-2219

Query Match 76.0%; Score 15.2; DB 15; Length 1284;
Best Local Similarity 85.0%; Pred. No. 3.3e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CTGATGCCCAACGAGCACC 20
DB 37 CTGATGCCCAACGAGCACC 56

RESULT 11
US-09-938-842A-2021/c
Sequence 2021, Application US/09938842A
Patent No. US20020160378A1
GENERAL INFORMATION:
APPLICANT: Harper, Jeff
APPLICANT: Kreps, Joel
APPLICANT: Wang, Xun
APPLICANT: Zhu, Tong
TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
TITLE OF INVENTION: SAME, AND METHODS OF USE
FILE REFERENCE: SCRIPI300-3
CURRENT APPLICATION NUMBER: US/09/938, 842A
CURRENT FILING DATE: 2001-08-24
PRIOR APPLICATION NUMBER: US 60/227,866
PRIOR FILING DATE: 2000-08-24
PRIOR APPLICATION NUMBER: US 60/264,647
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/300,111
PRIOR FILING DATE: 2001-06-22
NUMBER OF SEQ ID NOS: 5379
SEQ ID NO 2021
LENGTH: 1359
TYPE: DNA
ORGANISM: Arabidopsis thaliana
US-09-938-842A-2021

Query Match 76.0%; Score 15.2; DB 10; Length 1359;
Best Local Similarity 85.0%; Pred. No. 3.3e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CTGATGCCCAACGAGCACC 20
DB 132 CTGATGCCCAACGAGCACC 113

RESULT 12
US-09-938-842A-2021/c
Sequence 2021, Application US/09938842A
Publication No. US20040009476A9
GENERAL INFORMATION:
APPLICANT: Harper, Jeff
APPLICANT: Kreps, Joel
APPLICANT: Wang, Xun
APPLICANT: Zhu, Tong
TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
TITLE OF INVENTION: SAME, AND METHODS OF USE

FILE REFERENCE: SCRIPI300-3
CURRENT APPLICATION NUMBER: US/09/938, 842A
CURRENT FILING DATE: 2001-08-24
PRIOR APPLICATION NUMBER: US 60/227,866
PRIOR FILING DATE: 2000-08-24
PRIOR APPLICATION NUMBER: US 60/264,647
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/300,111
PRIOR FILING DATE: 2001-06-22
NUMBER OF SEQ ID NOS: 5379
SEQ ID NO 2021
LENGTH: 1359
TYPE: DNA
ORGANISM: Arabidopsis thaliana
US-09-938-842A-2021

Query Match 76.0%; Score 15.2; DB 12; Length 1359;
Best Local Similarity 85.0%; Pred. No. 3.3e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CTGATGCCCAACGAGCACC 20
DB 132 CTGATGCCCAACGAGCACC 113

RESULT 13
US-10-108-605-206
Sequence 206, Application US/10108605
Publication No. US20020160934A1
GENERAL INFORMATION:
APPLICANT: Broadus, Julie
APPLICANT: Stam, Lynn
APPLICANT: Bachmann, Jane
APPLICANT: Kamdar, Kim
TITLE OF INVENTION: NUCLEIC ACID SEQUENCES FROM DROSOPHILA MELANOGASTER THAT ENCODE
TITLE OF INVENTION: PROTEINS ESSENTIAL FOR LARVAL VIABILITY AND USES THEREOF
FILE REFERENCE: 31133B
CURRENT APPLICATION NUMBER: US/10/108,605
CURRENT FILING DATE: 2002-03-27
PRIOR APPLICATION NUMBER: US 09/761,142
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/176,418
PRIOR FILING DATE: 2000-01-14
NUMBER OF SEQ ID NOS: 361
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 206
LENGTH: 2031
TYPE: DNA
ORGANISM: Drosophila melanogaster
US-10-108-605-206

Query Match 76.0%; Score 15.2; DB 14; Length 2031;
Best Local Similarity 85.0%; Pred. No. 3.4e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CTGATGCCCAACGAGCACC 20
DB 695 CCGATGCCCAACGAGCACC 714

RESULT 14
US-09-815-242-6644
Sequence 6644, Application US/09815242
Patent No. US20020061569A1
GENERAL INFORMATION:
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari L.
APPLICANT: Zyskind, Judith W.
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John D.
APPLICANT: Carr, Grant J.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Xu, H. Howard

Search completed: February 12, 2004, 06:15:51
Job time : 120.659 secs

TITLE OF INVENTION: Identification of Essential Genes in
FILE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 6644
LENGTH: 2193
TYPE: DNA
ORGANISM: Enterococcus faecalis
FEATURE:
NAME/KEY: CDS
LOCATION: (1)...(2193)
US-09-815-242-6644

Query Match 76.0%; Score 15.2; DB 9; Length 2193;
Best Local Similarity 85.0%; Pred. No. 3.5e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CTGATCGCCAAAGCAGCAAC 20
DB 775 CTAATCGCAACAGCAAC 794

RESULT 15
US-10-108-605-116
Sequence 116, Application US/10108605
Publication No. US20020160934A1
GENERAL INFORMATION:
APPLICANT: Broadus, Julie
APPLICANT: Stam, Lynn
APPLICANT: Bachmann, Jane
APPLICANT: Kamdar, Kim
TITLE OF INVENTION: NUCLEIC ACID SEQUENCES FROM DROSOPHILA MELANOGASTER THAT ENCODE
FILE REFERENCE: 31133B
CURRENT APPLICATION NUMBER: US/10/108,605
CURRENT FILING DATE: 2002-03-27
PRIOR APPLICATION NUMBER: US 09/761,142
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/176,418
PRIOR FILING DATE: 2000-01-14
NUMBER OF SEQ ID NOS: 361
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 116
LENGTH: 2241
TYPE: DNA
ORGANISM: Drosophila melanogaster
US-10-108-605-116

Query Match 76.0%; Score 15.2; DB 14; Length 2241;
Best Local Similarity 85.0%; Pred. No. 3.5e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CTGATCGCCAAAGCAGCAAC 20
DB 783 CCGATCGCAACAGCCCAAC 802

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GenCore version 5.1.6
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OM nucleic - nucleic search, using SW model

Run on: February 12, 2004, 03:54:41 / Search time 1081.71 Seconds
(without alignments)
449.373 Million cell updates/sec

Title: US-09-692-077D-15
Perfect score: 20
Sequence: 1 ctgacgcacaaagagcaac 20

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 22781392 seqs, 12152238056 residues
Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: em_eatba:*
2: em_eatbam:*
3: em_eatlin:*
4: em_eatmu:*
5: em_eatov:*
6: em_eatpl:*
7: em_eatpro:*
8: em_eatrc:*
9: gb_eat1:*
10: gb_eat2:*
11: gb_eat3:*
12: gb_eat4:*
13: gb_eat5:*
14: gb_eat6:*
15: em_eatfun:*
16: em_eatcom:*
17: em_ges_hum:*
18: em_ges_inv:*
19: em_ges_pln:*
20: em_ges_vrt:*
21: em_ges_fun:*
22: em_ges_mam:*
23: em_ges_mus:*
24: em_ges_pro:*
25: em_ges_rtd:*
26: em_ges_phg:*
27: em_ges_vrl:*
28: gb_ges1:*
29: gb_ges2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	17.4	87.0	275 12	BI372571
2	16.8	84.0	428 28	BH756337
3	16.8	84.0	561 10	BE033222
4	16.8	84.0	700 10	BC636450

C	5	16.4	82.0	359	10	BC381314	BC381314	UI-R-CT0-
	6	16.4	82.0	597	14	N82961	N82961	TGSTRY53d1
	7	16.4	82.0	494	12	BI94631	BI94631	best28.5'
	8	16.4	82.0	700	28	BH962262	BH962262	cdg10b08
	9	16.4	82.0	749	28	BH674374	BH674374	BOMN43TF
	10	16.4	82.0	765	28	BH568386	BH568386	BOG1138TF
	11	16.4	82.0	794	28	BH537924	BH537924	BOGEB84TR
	12	16.4	82.0	806	28	BH694343	BH694343	BOHVA49TF
	13	16.4	82.0	892	29	AG071544	AG071544	Pan trogl
	14	16.4	82.0	936	14	CD255409	CD255409	AGENCOURT
	15	16.4	82.0	963	10	BC253789	BC253789	602366671
	16	16.4	80.0	1022	29	CNS044B1	CNS044B1	Teiraodon
	17	15.8	79.0	319	29	EX293512	EX293512	Arabidops
	18	15.8	79.0	324	29	EX293513	EX293513	Arabidops
	19	15.8	79.0	336	29	CNS00P16	CNS00P16	Arabidops
	20	15.8	79.0	360	29	C65542	C65542	Vuji
	21	15.8	79.0	379	12	BH284930	BH284930	BUT84930
	22	15.8	79.0	389	10	BF451274	BF451274	uz68a10.x
	23	15.8	79.0	411	10	BF440154	BF440154	MLG0557
	24	15.8	79.0	417	9	AI018990	AI018990	SME5T0630
	25	15.8	79.0	418	28	BH755131	BH755131	SALK 0484
	26	15.8	79.0	437	10	BR072723	BR072723	NCSM4C8T7
	27	15.8	79.0	458	29	AC256246	AC256246	Lotus jap
	28	15.8	79.0	478	12	BP026586	BP026586	BP026586
	29	15.8	79.0	481	10	BE484918	BE484918	171738 BA
	30	15.8	79.0	487	12	BI426448	BI426448	sag03d05
	31	15.8	79.0	507	9	AL587025	AL587025	AL587025
	32	15.8	79.0	513	9	AJ396379	AJ396379	AJ396379
	33	15.8	79.0	517	10	BF457549	BF457549	UI-M-B21-
	34	15.8	79.0	533	13	BU856446	BU856446	603600053
	35	15.8	79.0	535	12	BI974374	BI974374	sal19b01
	36	15.8	79.0	540	9	AI976827	AI976827	EST271509
	37	15.8	79.0	553	12	BM525002	BM525002	sal26f07
	38	15.8	79.0	558	12	BM328798	BM328798	PIC1_26_F
	39	15.8	79.0	574	13	BQ770626	BQ770626	UI-M-F10-
	40	15.8	79.0	590	28	BH365931	BH365931	CH230-60K
	41	15.8	79.0	594	28	BH777488	BH777488	fzmb013f0
	42	15.8	79.0	603	14	CB526603	CB526603	UI-M-FY0-
	43	15.8	79.0	622	28	BH199984	BH199984	Sml-46R16
	44	15.8	79.0	622	28	AQ399921	AQ399921	mgxb00003M
	45	15.8	79.0	633	12	BU122635	BU122635	BU122635

ALIGNMENTS

RESULT 1
BI372571
LOCUS
DEFINITION RE59566, Sprime RE Drosophila melanogaster normalized Embryo pFLc-1
Drosophila melanogaster cDNA clone RE59566 5, mRNA sequence.
BI372571
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
1 (bases 1 to 275)
Stapleton, M., Brkstein, P., Hong, L., Tyler, D., Berman, B., Carlson, J., Champe, M., Chavez, C., Dorsett, V., Farfan, D., Frie, E., George, R., Gonzalez, M., Guarin, H., Harris, N., Li, P., Liao, G., Mistr, S., Mungall, C. J., Nunoo, J., Pacled, J., Paragas, V., Park, S., Phouanavong, S., Wan, K., Yu, C., Lewis, S. E., Celinker, S. and Rubin, G. M.
BDGP/HMI RE Drosophila EST Project
Unpublished
Contact: Stapleton, M.
BDGP
Lawrence Berkeley National Lab
One Cyclotron Rd, Berkeley, CA 94720, USA
Fax: 510 486 6798

TITLE
JOURNAL
COMMENT

Email: http://www.fruitfly.org/EST_est@fruitfly.berkeley.edu
 Plate: RE:595 Row: F Column: 6
 High quality sequence stop: 246.
 Location/Qualifiers

FEATURES

source

1. 275
 /organism="Drosophila melanogaster"
 /mol_type="mRNA"
 /db_xref="taxon:7227"
 /clone="RE59566"
 /sex="male and female"
 /dev_stage="0-24 hours mixed stage embryonic"
 /lab_host="DHS-alpha Tona"
 /clone_lib="RE Drosophila melanogaster normalized Embryo
 pRc-1"
 /note="Organ: embryo; Vector: pRc1, Site 1: XhoI; Site 2:
 BamHI; Library was kindly generated by Piero Carninci at
 the RIKEN. The library was normalized and excised using
 Cre recombinase. Plasmid cDNA library."

BASE COUNT

77 a 74 c 67 g 57 t
 Query Match 87.0%; Score 17.4; DB 12; Length 275;
 Best Local Similarity 94.7%; Pred. No. 1.3e+02;
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 CTGATCGCCAAACGACGA 19
 DB 178 CTGATCGCCAAACGACGA 196

RESULT 2

LOCUS BH756337 428 bp DNA linear GSS 01-MAR-2002
 DEFINITION SALK_053523.55.75.x Arabidopsis thaliana TDNA insertion lines
 Arabidopsis thaliana genomic clone SALK_053523.55.75.x, genomic
 survey sequence.
 BH756337
 BH756337.1 GI:19038548
 GSS.
 Arabidopsis thaliana (thale cress)
 Arabidopsis thaliana
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; rosids
 ; euroside II; Brassicales; Brassicaceae; Arabidopsie.
 1 (bases 1 to 428)
 Alonso,J.M., Leisner,T.J., Barajas,P., Chen,H., Cheuk,R., Gadrinab
 ,C., Jeske,A., Karsne,W., Kim,C.O., Parker,H., Prednis,L., Shinn,P.
 , Zimmerman,U. and Ecker,J.R.
 A Sequence-Indexed Library of Insertion Mutations in the
 Arabidopsis Genome
 Unpublished

REFERENCE
 AUTHORS
 TITLE

JOURNAL

COMMENT
 Contact: Joseph R. Ecker
 Salt Institute Genomic Analysis Laboratory (SIGNAL)
 The Salt Institute for Biological Studies
 10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
 Tel: 858 453 4100 x1752
 Fax: 858 558 6379
 Email: ecker@salt.edu

This is single pass sequence recovered from the left border of
 TDNA.
 Class: TDNA tagged.

FEATURES

source

Location/Qualifiers
 1. 428
 /organism="Arabidopsis thaliana"
 /mol_type="genomic DNA"
 /strain="Columbia 0"
 /db_xref="taxon:3702"
 /clone="SALK_053523.55.75.x"
 /clone_lib="Arabidopsis thaliana TDNA insertion lines"
 /note="PCR was performed on Arabidopsis thaliana lines
 each of which contains one or more TDNA insertion
 elements. The resultant fragment for each line was
 directly sequenced to determine the genomic sequence at

the site of insertion. Details of the protocols used can
 be found at http://signal.salk.edu/cdna_protocols.html"

BASE COUNT

95 a 86 c 101 g 146 t
 Query Match 84.0%; Score 16.8; DB 28; Length 428;
 Best Local Similarity 90.0%; Pred. No. 3.1e+02;
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 CTGATCGCCAAACGACGAC 20
 DB 401 CTGATCGCCAAACGACGAC 382

RESULT 3

LOCUS BE033222 561 bp mRNA linear EST 09-JUL-2000
 DEFINITION 133577 MARC 1P1G Sus scrofa cDNA 5', mRNA sequence.
 ACCESSION BE033222
 VERSION BE033222.1 GI:8328231
 KEYWORDS EST.
 SOURCE Sus scrofa (pig)
 ORGANISM Sus scrofa
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 1 (bases 1 to 561)
 Fahrenkrug,S.C., Smith,T.P.L., Freking,B.A., Cho,J., White,J.,
 Vallet,J., Wise,T., Rohrer,G.A., Perlea,G., Sultana,R., Quackenbush
 J. and Keefe,J.W.
 Porcine gene discovery by normalized cDNA-library sequencing and
 EST cluster assembly
 Mamm. Genome 13 (8), 475-478 (2002)
 22213789
 12226715
 Contact: Smith TPL
 USDA, ARS, US Meat Animal Research Center
 PO Box 166, Clay Center, NE 68933-0166, USA
 Tel: 402 762 4366
 Fax: 402 762 4390
 Email: smith@mail.marc.usda.gov
 Single pass sequencing. Bases called and alt trimmed with phred
 v0.980904.e. Vector identified by cross_match with the -mnscore 18
 and -mismatch 12 options.
 PCR Primers
 FORWARD: AGGAAACAGCTATGACCAT
 BACKWARD: GTTTCACAGTCACGACG
 Plate: 68 Row: L Column: 5
 Seq primer: ATTGAGTGCACCTATAG.
 Location/Qualifiers

FEATURES

source

1. 561
 /organism="Sus scrofa"
 /mol_type="mRNA"
 /db_xref="taxon:9823"
 /tissue_type="pooled"
 /lab_host="DH10B"
 /clone_lib="MARC 1P1G"
 /note="Vector: PCMV SPOR16; Site 1: NotI; Site 2: SalI;
 Library made from pooled tissue from day 11, 13, 15, 20,
 and 30 embryos."
 This is single pass sequence recovered from the left border of
 TDNA.
 Class: TDNA tagged.

BASE COUNT

130 a 179 c 135 g 117 t
 Query Match 84.0%; Score 16.8; DB 10; Length 561;
 Best Local Similarity 90.0%; Pred. No. 3.4e+02;
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 CTGATCGCCAAACGACGAC 20
 DB 303 CTGATCGCCAAACGACGAC 322

RESULT 4

BG636450

LOCUS BG636450 700 bp mRNA linear EST 23-APR-2001
 DEFINITION SD14169.Sprtime SD Drosophila melanogaster Schneider L2 cell culture
 POT2 Drosophila melanogaster cDNA clone SD14169 5 similar to
 CG17503: FBan0017509 located on: 2R 48E2-48E2; 04/13/2001, mRNA
 sequence.

ACCESSION BG636450
 VERSION BG636450.1 GI:13763987
 KEYWORDS EST.
 SOURCE Drosophila melanogaster (fruit fly)
 ORGANISM Drosophila melanogaster
 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 Ephyridiida; Drosophilidae; Drosophila.
 1 (bases 1 to 700)
 Harvey, D., Brokstein, P., Hong, L., Evans-Holm, M., Su, C., Tsang, G.,
 Lewis, S. and Rubin, G. M.
 BDCP/HMT Drosophila EST Project
 Unpublished
 Contact: Stapleton, M.
 BDCP
 Lawrence Berkeley National Lab
 One Cyclotron Rd. Berkeley, CA 94720, USA
 Fax: 510 486 6798
 Email: http://www.fruitfly.org/EST_estefruitfly.berkeley.edu
 hit genomic AE003823: arm:2R [6997351,7260081]
 estimated-cyto:48D8-48F5: 04/13/2001
 Plate: SD 141 row: F column: 9
 High quality sequence stop: 636.
 Location/Qualifiers
 1..700
 /organism="Drosophila melanogaster"
 /mol_type="mRNA"
 /db_xref="taxon:7227"
 /clone="SD14169"
 /lab_host="DHS-alpha"
 /clone_1lb="SD Drosophila melanogaster Schneider L2 cell
 culture POT2"
 /note="Vector: POT2; Site 1: EcoRI; Site 2: XhoI; Sized
 fractionated cDNAs were directly ligated into POT2.
 Plasmid cDNA library."

BASE COUNT 196 a 186 c 173 g 145 t
 ORIGIN

Query Match 84.0%; Score 16.8; DB 10; Length 700;
 Best Local Similarity 90.0%; Pred. No. 3.7e+02;
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CTGATGCCCAACGAGCAAC 20
 DB 232 CTGATGCCCAACGAGCAAC 251

RESULT 5
 LOCUS BG381314/c 359 bp mRNA linear EST 12-MAR-2001
 DEFINITION UI-R-CTO-pui-g-04-0-UI-81 UI-R-CTO Rattus norvegicus cDNA clone
 UI-R-CTO-pui-g-04-0-UI 3', mRNA sequence.
 ACCESSION BG381314
 VERSION BG381314.1 GI:13305786
 KEYWORDS EST.
 SOURCE Rattus norvegicus (Norway rat)
 ORGANISM Rattus norvegicus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
 Rattus.
 1 (bases 1 to 359)
 Bonaldo, M. F., Lennon, G. and Soares, M. B.
 Normalization and subtraction: two approaches to facilitate gene
 discovery
 Genome Res. 6 (9), 791-806 (1996)
 JOURNAL MEDLINE
 PUBMED 8889548
 COMMENT Contact: Soares, MB

Coordinated Laboratory for Computational Genomics
 University of Iowa
 375 Newton Road, 4156 MEBRF, Iowa City, IA 52242, USA
 Tel: 319 335 8250
 Fax: 319 335 9565
 Email: bento-soares@uiowa.edu
 The sequence contained an oligo-dT track that was present in the
 oligonucleotide that was used to prime the synthesis of first
 strand cDNA and therefore this may represent a bonafide poly A
 tail. cDNA Library Preparation: M.B. Soares Lab Clone distribution:
 clones will be available through Research Genetics (www.resgen.com)
 The following repetitive elements were found in this cDNA sequence:
 73-206, >RSINE1\$INE/B4(B5)
 Seg primer: M13 Forward
 POLYA=yes.

FEATURES
 source
 Location/Qualifiers
 1..359
 /organism="Rattus norvegicus"
 /mol_type="mRNA"
 /strain="Sprague-Dawley"
 /db_xref="taxon:10116"
 /clone="UI-R-CTO-pui-g-04-0-UI"
 /dev_stage="ADULT"
 /lab_host="DH10B (Life Technologies)"
 /clone_1lb="UI-R-CTO"
 /note="Vector: p773D-Pac (Pharmacia) with a modified
 polylinker: Site_1: Not I; Site_2: Eco RI; The UI-R-CTO
 library is a normalized library constructed from the
 following rat brain tissues: embryonic day 17, embryonic
 day 19, embryonic day 21, adult day 1, adult day 12, adult
 day 75, adult day 200. For a detailed description of the
 library from which this clone was derived, please visit
 our web site at ratat.eng.uiowa.edu. The subtraction has
 been previously described in (Bonaldo, Lennon and Soares,
 Genome Research 6:791-806, 1996)
 TAG_SBO=None found"

BASE COUNT 73 a 96 c 71 g 119 t
 ORIGIN

Query Match 82.0%; Score 16.4; DB 10; Length 359;
 Best Local Similarity 94.4%; Pred. No. 4.7e+02;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CTGATGCCCAACGAGCA 18
 DB 112 CTGATGCCCAACGAGCA 95

RESULT 6
 LOCUS N82961 477 bp mRNA linear EST 22-MAY-2000
 DEFINITION TgESTzy53d12.r1 TgrH Tachyzoite cDNA Toxoplasma gondii cDNA clone
 Tgzy53d12.r1 5', mRNA sequence.
 ACCESSION N82961
 VERSION N82961.1 GI:1258714
 KEYWORDS EST.
 SOURCE Toxoplasma gondii
 ORGANISM Toxoplasma gondii
 Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida;
 Sarcocystidae; Toxoplasma.
 1 (bases 1 to 477)
 Hehl, A., Manger, I., Marra, M., Sibley, L. D., Ajioke, J. A., Aslett, M. A.,
 Dietrich, N., Dubuque, T., Hillier, L., Kucaba, T., Wan, K. L.,
 Waterston, R. H. and Boothroyd, J.
 WashU-Merck-Stanford-NIH Toxoplasma EST project
 Unpublished
 Contact: Marra M
 WashU-Merck EST Project
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: toxow@watsbn.wustl.edu

David Sibley at toxoest@orcim.wustl.edu for further information relating to organism, clone or library availability.
Seq primer: T3
High quality sequence stop: 301.
Location/Qualifiers

FEATURES

source

```

1..477
/organism="Toxoplasma gondii"
/mol_type="mRNA"
/strain="RH"
/db_xref="taxon:5811"
/clone="cgzy53d12.r1"
/lab_host="XLI-Blue MRF"
/clone_lib="Tigr1 Tachyzoite cDNA"
/notes="Vector: Lambda ZAP, Site_1: EcoRI, Site_2: XhoI; Toxoplasma RH strain tachyzoites were grown in human foreskin fibroblast cultures in vitro. The library was constructed by K.L. Wan, Cambridge University. cDNAs were synthesized from polyA RNAs by oligo d(T) priming and directionally cloned into the EcoRI to XhoI sites of the Lambda ZAPIT vector using the ZAP-cDNA synthesis kit (Stratagene). WARNING: the library contains a small percentage of cDNAs derived from the human host cells."
BASE COUNT      104 a      107 c      146 g      109 t      11 others
ORIGIN

```

Query Match 82.0%; Score 16.4; DB 14; Length 477;
Best Local Similarity 94.4%; Pred. No. 5.2e+02; Indels 0; Gaps 0;
Matches 17; Conservative 0; Mismatches 1;

OY 2 TGATGCCAAGAGCA 19
DB 383 TGATTGCCAAGAGCA 400

RESULT 7 594 bp mRNA linear EST 19-OCT-2001
B1946431
LOCUS BEST28.5' Honeybee brain cDNA library Apis mellifera cDNA 5', mRNA
DEFINITION
B1946431
ACCESSION
B1946431
VERSION
B1946431.1 GI:16285097
KEYWORDS
EST.
SOURCE
Apis mellifera (honeybee)
ORGANISM
Apis mellifera
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Apoidea; Apidae; Apis.
1 (bases 1 to 594)
Kucharski, R. and Maleszka, R.
Evaluation of differential gene expression during behavioral development in the honeybee using microarrays and northern blots
Genome Biol. 3 (2), research0007.1-9 (2002)
21853287
11864369
Other ESTs: BEST28.3'
Contact: Maleszka R
Visual Sciences Group
Research School of Biological Sciences, Australian National University
Biology Pl., Canberra ACT 0200, Australia
Tel: +61 2 6125 0451
Fax: +61 2 6125 3784
Email: maleszka@rsbs.anu.edu.au
Seq primer: M13 reverse.

FEATURES

source

```

1..594
/organism="Apis mellifera"
/mol_type="mRNA"
/db_xref="taxon:7460"
/sex="female"
/tissue_type="central brain, mushroom bodies, central body
, deutocerebrum"
/dev_stage="adult worker"

```

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/lab_host="E.coli SOLR"
/clone_lib="Honeybee brain cDNA library"
/notes="Organism: brain; Vector: pBluescript II SK-; Site_1: EcoRI, Site_2: XhoI; cDNA-harboring phagemids were obtained by performing mass excision procedure on honeybee brain cDNA lambda Unizap XR library (Ebert P.R. et al., 1998, Insect Mol. Biol. 7(2):151-62)."

```

BASE COUNT

```

161 a      132 c      184 g      117 t
ORIGIN

```

Query Match 82.0%; Score 16.4; DB 12; Length 594;
Best Local Similarity 94.4%; Pred. No. 5.7e+02; Indels 0; Gaps 0;
Matches 17; Conservative 0; Mismatches 1;

OY 2 TGATGCCAAGAGCA 19
DB 394 TGATGCCAAGAGCA 411

RESULT 8 700 bp DNA linear GSS 01-OCT-2002
BH962262
LOCUS odg10b08.b1 B.oleracea002 Brassica oleracea genomic, genomic survey
DEFINITION
BH962262
ACCESSION
BH962262
VERSION
BH962262.1 GI:23443488
KEYWORDS
GSS.
SOURCE
Brassica oleracea
ORGANISM
Brassica oleracea
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids
; eurosids II; Brassicales; Brassicaceae; Brassica.
1 (bases 1 to 700)
Delehaunty, K., Fewell, G., Fulton, L., McCombie, W.R., Miner, T., Nash
, W., Rabinowicz, P.D. and Wilson, R.K.
Whole genome shotgun reads from Brassica oleracea
Unpublished
Contact: Richard K. Wilson
Genome Sequencing Center
Washington University School of Medicine
Email: submissions@watson.wustl.edu
Plate: odg10 row: b column: 08
Seq primer: -21UPOT forward
Class: Shotgun
High quality sequence start: 20
High quality sequence stop: 541.
Location/Qualifiers

FEATURES

source

```

1..700
/organism="Brassica oleracea"
/mol_type="genomic DNA"
/db_xref="taxon:3712"
/clone_lib="B.oleracea002"
/notes="Vector: pOTW13; Whole genome shotgun library from flowering buds. DNA was purified from a crude nuclear prep using Brassica oleracea TO1000DH3 buds provided by Thomas Osborn at the University of Wisconsin. Genomic DNA was provided by Pablo Rabinowicz (CSHL) and the shotgun library prepared at Washington University Genome Sequencing Center."

```

BASE COUNT 190 a 197 c 137 t 1 others
ORIGIN

Query Match 82.0%; Score 16.4; DB 28; Length 700;
Best Local Similarity 94.4%; Pred. No. 6e+02; Indels 0; Gaps 0;
Matches 17; Conservative 0; Mismatches 1;

OY 2 TGATGCCAAGAGCA 19
DB 222 TGATGCCAAGAGCA 239

RESULT 9
BH674374/c

LOCUS BH674374 749 bp DNA linear GSS 19-FEB-2002
 DEFINITION BOMNJ43TF BO_2_3 KB Brassica oleracea genomic clone BOMNJ43,
 genomic survey sequence.
 ACCESSION BH674374
 VERSION BH674374.1 GI:18743024
 KEYWORDS GSS.
 SOURCE Brassica oleracea
 ORGANISM Brassica oleracea
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids
 ; euroside II; Brassicales; Brassicaceae; Brassica.
 1 (bases 1 to 749)
 Town,C.D., Van Aken,S., Uteerback,T., Koo,H. and Fraser,C.M.
 Whole genome shotgun sequencing of Brassica oleracea
 Unpublished
 CONTACT: Chris Town
 TIGR
 9712 Medical Center Drive, Rockville, MD 20850, USA.
 Tel: 301-838-3523
 Fax: 301-838-0208
 Email: cdtown@tigr.org
 DNA is from a doubled haploid provided by Tom Osborn.
 Seg primer: TF
 Class: sheared ends.

FEATURES
 source
 1..749
 /organism="Brassica oleracea"
 /mol_type="genomic DNA"
 /strain="TO1000DH3"
 /db_xref="taxon:3712"
 /clone_1ib="BOMNJ43"
 /note="Vector: pHO51; Site 1: BactI; 2-3 kb sheared
 genomic DNA inserted into pHO51 using BactI linkers"

BASE COUNT 154 a 190 c 191 g 214 t
 ORIGIN

Query Match 82.0%; Score 16.4; DB 28; Length 749;
 Best Local Similarity 94.4%; Pred. No. 6.2e+02;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 TGATGCCCAACGACCAA 19
 |||
 DB 665 TGTTCGCCAAGACGACCA 648

RESULT 10
 LOCUS BH568386 765 bp DNA linear GSS 14-DEC-2001
 DEFINITION BOGY138TF BOGY Brassica oleracea genomic clone BOGY138, genomic
 survey sequence.
 ACCESSION BH568386
 VERSION BH568386.1 GI:17820226
 KEYWORDS GSS.
 SOURCE Brassica oleracea
 ORGANISM Brassica oleracea
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids
 ; euroside II; Brassicales; Brassicaceae; Brassica.
 1 (bases 1 to 765)
 Town,C.D., Van Aken,S., Uteerback,T., Koo,H. and Fraser,C.M.
 Whole genome shotgun sequencing of Brassica oleracea
 Unpublished
 Other_GSS: BOGY138TF
 CONTACT: Chris Town
 TIGR
 9712 Medical Center Drive, Rockville, MD 20850, USA.
 Tel: 301-838-3523
 Fax: 301-838-0208
 Email: cdtown@tigr.org
 DNA is from a doubled haploid provided by Tom Osborn.
 Seg primer: TF
 Class: sheared ends.

FEATURES
 source
 Location/Qualifiers
 1..765
 /organism="Brassica oleracea"
 /mol_type="genomic DNA"
 /strain="TO1000DH3"
 /db_xref="taxon:3712"
 /clone_1ib="BOGY138"
 /note="Vector: pHO51; Site 1: BactI; 2-3 kb sheared
 genomic DNA inserted into pHO51 using BactI linkers"

BASE COUNT 158 a 161 c 225 g 221 t
 ORIGIN

Query Match 82.0%; Score 16.4; DB 28; Length 765;
 Best Local Similarity 94.4%; Pred. No. 6.2e+02;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 TGATGCCCAACGACCAA 19
 |||
 DB 68 TGTTCGCCAAGACGACCA 51

RESULT 11
 BH537924 794 bp DNA linear GSS 14-DEC-2001
 LOCUS BOGE84TR BOGY Brassica oleracea genomic clone BOGE84, genomic
 survey sequence.
 ACCESSION BH537924
 VERSION BH537924.1 GI:17776032
 KEYWORDS GSS.
 SOURCE Brassica oleracea
 ORGANISM Brassica oleracea
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids
 ; euroside II; Brassicales; Brassicaceae; Brassica.
 1 (bases 1 to 794)
 Town,C.D., Van Aken,S., Uteerback,T., Koo,H. and Fraser,C.M.
 Whole genome shotgun sequencing of Brassica oleracea
 Unpublished
 Other_GSS: BOGE84TR
 CONTACT: Chris Town
 TIGR
 9712 Medical Center Drive, Rockville, MD 20850, USA.
 Tel: 301-838-3523
 Fax: 301-838-0208
 Email: cdtown@tigr.org
 DNA is from a doubled haploid provided by Tom Osborn.
 Seg primer: TF
 Class: sheared ends.

FEATURES
 source
 Location/Qualifiers
 1..794
 /organism="Brassica oleracea"
 /mol_type="genomic DNA"
 /strain="TO1000DH3"
 /db_xref="taxon:3712"
 /clone_1ib="BOGE84"
 /note="Vector: pHO51; Site 1: BactI; 2-3 kb sheared
 genomic DNA inserted into pHO51 using BactI linkers"

BASE COUNT 241 a 221 c 170 g 162 t
 ORIGIN

Query Match 82.0%; Score 16.4; DB 28; Length 794;
 Best Local Similarity 94.4%; Pred. No. 6.3e+02;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 TGATGCCCAACGACCAA 19
 |||
 DB 631 TGTTCGCCAAGACGACCA 648

RESULT 12
 BH694343/c

LOCUS BH694343 806 bp DNA linear GSS 19-FEB-2002
 DEFINITION BOHVA49TF BO_2.3_KB Brassica oleracea genomic clone BOHVA49,
 genomic survey sequence.
 ACCESSION BH694343
 VERSION BH694343.1 GI:18764923
 KEYWORDS GSS.
 SOURCE Brassica oleracea
 ORGANISM Brassica oleracea
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids
 ; eurosids II; Brassicales; Brassicaceae; Brassica.
 1 (bases 1 to 806)
 Town, C.D., Van Aken, S., Uteerback, T., Koo, H. and Frazer, C.M.
 Whole genome shotgun sequencing of Brassica oleracea
 Unpublished
 JOURNAL Contact: Chris Town
 TIGR
 9712 Medical Center Drive, Rockville, MD 20850, USA.
 Tel: 301-838-3523
 Fax: 301-838-0208
 Email: cdtown@tigr.org
 DNA is from a doubled haploid provided by Tom Osborn.
 Seq primer: TP
 Class: sheared ends.
 Location/Qualifiers
 1..806
 /organism="Brassica oleracea"
 /mol_type="genomic DNA"
 /strain="T01000DH3"
 /db_xref="taxon:3712"
 /clone="BOHVA49"
 /clone_1lb="BO_2.3_KB"
 /note="Vector: PHOS1, Site 1: BstXI, 2-3 kb sheared
 genomic DNA inserted into PHOS1 using BstXI linkers"

BASE COUNT 168 a 167 c 239 g 232 t

ORIGIN

Query Match 82.0%; Score 16.4; DB 28; Length 806;
 Best Local Similarity 94.4%; Pred. No. 6.4e+02;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 TGTGCGCAACGAGCAA 19
 ||||||||||||||||
 115 TGTGCGCAACGAGCAA 98

RESULT 13
 AG071544 892 bp DNA linear GSS 03-NOV-2001
 LOCUS Pan troglodytes DNA, clone: PTB-062M08.R, genomic survey sequence.
 DEFINITION AG071544
 ACCESSION AG071544.1 GI:16623346
 KEYWORDS GSS.
 SOURCE Pan troglodytes (chimpanzee)
 ORGANISM Pan troglodytes
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Pan.
 1
 Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T.,
 Tokoki, Y., Watanabe, H. and Sakaki, Y.
 BAC end sequences of library PTB
 Unpublished
 2 (bases 1 to 892)
 Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T.,
 Tokoki, Y., Watanabe, H. and Sakaki, Y.
 Direct Submission
 Submitted (02-AUG-2001) Aao, Fujiyama, The Institute of Physical
 and Chemical Research (RIKEN), Genomic Sciences Center (GSC),
 1-7-22, Shinto-chou, Tsukumi-ku, Yokohama, Kanagawa 230-0045, Japan
 (E-mail: shintob@sc.riken.go.jp, URL: http://hgp.gsc.riken.go.jp/
 Tel: 81-45-503-9111, Fax: 81-45-503-9170)
 Clones are derived from the chimpanzee BAC library PTB This BAC end
 was generated during the Rad process and may have higher chance of

COMMENT

clone tracking errors.
 PRIMERS
 Sequencing: MJ3Rev
 LIBRARY
 Vector : pKS145
 R.site 1 : SacI
 R.site 2 : SacI.
 Location/Qualifiers
 1..892
 /organism="Pan troglodytes"
 /mol_type="genomic DNA"
 /db_xref="taxon:9598"
 /clone="PTB-062M08.R"
 /sex="male"
 /cell_type="lymphoblast"
 /clone_1lb="PTB Chimpanzee Male BAC Library"

BASE COUNT 300 a 351 c 211 g 23 t

ORIGIN

Query Match 82.0%; Score 16.4; DB 29; Length 892;
 Best Local Similarity 94.4%; Pred. No. 6.6e+02;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 GATGCCCAACGAGCAAC 20
 ||||||||||||||||
 711 GATGCCCAACGAGCAAC 728

RESULT 14
 CD255409 936 bp mRNA linear EST 22-MAY-2003
 LOCUS AGNCOURT 14164603 NICHD_XGC_Brl1 Xenopus laevis cDNA clone
 DEFINITION IMAGE:6951820 5', mRNA sequence.
 ACCESSION CD255409
 VERSION CD255409.1 GI:31015875
 KEYWORDS EST.
 SOURCE Xenopus laevis (African clawed frog)
 ORGANISM Xenopus laevis
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
 Xenopodidae; Xenopus.
 1 (bases 1 to 936)
 NIH-MGC http://mgc.ncl.nih.gov/.
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished
 Contact: Daniela S. Gerhard, Ph.D.
 Office of Cancer Genomics / NIH
 Bldg. 31 Rm10A07 Bethesda, MD 20892
 Email: cgabs-r@mail.nih.gov
 Tissue Procurement:
 cDNA Library Preparation: Life Technologies, Inc.
 DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 plate: LLNL4571 row: 1 column: 03
 High quality sequence strop: 534.
 Location/Qualifiers
 1..936
 /organism="Xenopus laevis"
 /mol_type="mRNA"
 /db_xref="taxon:8355"
 /clone="IMAGE:6951820"
 /dev_stage="adult"
 /lab_host="DH10B (phage-resistant)"
 /clone_1lb="NICHD_XGC_Brl1"
 /note="Organ: brain; Vector: pCMV-SPORT6; Site 1: NotI;
 Site 2: SalI; Cloned unidirectionally. Primer: Oligo dt.
 Average insert size 1.5 kb. Constructed by Life
 Technologies. Note: This is a Xenopus Gene Collection (XGC
) library."

BASE COUNT 270 a 190 c 225 g 251 t
ORIGIN

Query Match 82.0%; Score 16.4; DB 14; Length 936;
Best Local Similarity 94.4%; Pred. No. 6.7e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 GATCGCAACGAGCAGC 20
|||||
DB 519 GATCGCAACGAGCAGC 536

RESULT 15
BG253789 963 bp mRNA linear EST 13-FEB-2001
LOCUS 602366671p1 NIH_MGC_91 Homo sapiens cDNA clone IMAGE:4474961 5',
DEFINITION
MRNA sequence.

ACCESSION BG253789
VERSION BG253789.1 GI:12763605
KEYWORDS
EST.
SOURCE
ORGANISM Homo sapiens (human)

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE 1 (bases 1 to 963)
JOURNAL NIH-MGC http://mgs.nci.nih.gov/.
COMMENT National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished
Contact: Robert Strausberg, Ph.D.
Email: cgabbs-romail.nih.gov
Tissue Procurement: DCTD/DRP
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Place: LHM10299 row: n column: 18
High quality sequence stop: 666.
Location/Qualifiers

FEATURES
source 1..963
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4474961"
/tissue_type="adenocarcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_1lb="NIH_MGC_91"
/note="Organ: prostate; Vector: PCMV-SPORT6; Site 1: NotI;
Site 2: SalI; Cloned unidirectionally; oligo-dT primed.
Average insert size 1.4 kb. Library enriched for
full-length clones and constructed by life technologies.
Note: this is a NIH_MGC Library."

BASE COUNT 328 a 226 c 208 g 200 t
ORIGIN 1 others

Query Match 82.0%; Score 16.4; DB 10; Length 963;
Best Local Similarity 94.4%; Pred. No. 6.8e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 GATCGCAACGAGCAGC 20
|||||
DB 776 GATCGCAACGAGCAGC 793

Search completed: February 12, 2004, 06:05:58
Job time : 1087.71 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 12, 2004, 01:54:29 / Search time 585.854 Seconds
(without alignments)
1396.582 Million cell updates/sec

Title: US-09-692-077D-16

Perfect score: 20

Sequence: 1 aaagacgaatgacacacag 20

Scoring table: IDENTITY_NUC

Gapop 10.0, Gapext 1.0

Searched: 2888711 seqs, 2045481386 residues

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Database:

GeneB1:

1: gb_da:*

2: gb_hcg:*

3: gb_in:*

4: gb_cm:*

5: gb_ov:*

6: gb_pac:*

7: gb_ph:*

8: gb_pl:*

9: gb_pr:*

10: gb_ro:*

11: gb_scb:*

12: gb_ey:*

13: gb_un:*

14: gb_vl:*

15: em_ba:*

16: em_fun:*

17: em_hum:*

18: em_in:*

19: em_mu:*

20: em_om:*

21: em_or:*

22: em_ov:*

23: em_pat:*

24: em_ph:*

25: em_pl:*

26: em_ro:*

27: em_scb:*

28: em_un:*

29: em_vl:*

30: em_hcg_hum:*

31: em_hcg_hmv:*

32: em_hcg_other:*

33: em_hcg_mus:*

34: em_hcg_pin:*

35: em_hcg_rtd:*

36: em_hcg_mam:*

37: em_hcg_vrt:*

38: em_hcg_hum:*

39: em_hcg_mus:*

40: em_hcg_other:*

41: em_hcg_other:*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	20	100.0	20	AX350504	AX350504 Sequence
2	20	100.0	885	HUMRA2C2	M38742 Human alpha
3	20	100.0	1344	AX350490	AX350490 Sequence
4	20	100.0	1344	AF316895	AF316895 Homo sapi
5	20	100.0	1353	AX350489	AX350489 Sequence
6	20	100.0	2072	AR270618	AR270618 Sequence
7	20	100.0	2072	HUMADRA2RA	M34041 Human alpha
8	20	100.0	3274	AX548756	AX548756 Sequence
9	20	100.0	9842	AF005900	AF005900 Homo sapi
10	20	100.0	22842	AC092603	AC092603 Homo sapi
11	18.4	92.0	1168	PV1251176	AJ251176 Phoca vit
12	18.4	92.0	1174	SSC251177	AJ251177 Sus scrofa
13	18.4	92.0	1185	ASP427259	AJ27259 Anomaluru
14	18.4	92.0	149169	AL840630	AL840630 Zebrafish
15	18.4	92.0	171406	BX510991	BX510991 Danto rer
16	17.4	87.0	238	BX323232	BX323232 Arabidops
17	17.4	87.0	1171	DDAAR2B	Y15947 Dugong dugo
18	17.4	87.0	1185	AF337541	AF337541 Tonatia b
19	17.4	87.0	1203	TTB315939	AF15939 Tapirus t
20	17.4	87.0	45740	AC012972	AC012972 Drosophi
21	17.4	87.0	62054	AF161800	AF161800 Homo sapi
22	17.4	87.0	77521	F7H2	AC034256 Sequence
23	17.4	87.0	95359	AC078903	AC078903 Homo sapi
24	17.4	87.0	109219	AF159227	AF159227 Homo sapi
25	17.4	87.0	132063	AC017096	AC017096 Homo sapi
26	17.4	87.0	155132	AC080148	AC080148 Homo sapi
27	17.4	87.0	159032	AC083843	AC083843 Homo sapi
28	17.4	87.0	164752	AC116696	AC116696 Mus muscu
29	17.4	87.0	168583	AC104510	AC104510 Drosophi
30	17.4	87.0	180919	AC007521	AC007521 Drosophi
31	17.4	87.0	189652	BX537119	BX537119 Danto rer
32	17.4	87.0	283075	AB003485	AB003485 Drosophi
33	17.4	87.0	334028	AC116537	AC116537 Drosophi
34	17	85.0	193800	AC126994	AC126994 Rattus no
35	17	85.0	255782	AC106301	AC106301 Rattus no
36	16.8	84.0	1149	RAM315937	AJ15937 Roussetus
37	16.8	84.0	1152	DSA427263	AJ427263 Dipus sag
38	16.8	84.0	1153	EM42ABREC	Y12525 Elephas max
39	16.8	84.0	1159	AM42ABREC	Y12526 Amdilyomus
40	16.8	84.0	1162	FCB251174	AJ251174 Felis cat
41	16.8	84.0	1172	ARU427256	AJ427256 Apidontoni
42	16.8	84.0	1176	TSW427267	AJ427267 Thyromomy
43	16.8	84.0	1180	CRO271336	AJ271336 Cavia por
44	16.8	84.0	1183	DR0419811	AJ419811 Desmodus
45	16.8	84.0	1197	LCR427254	AJ427254 Lepus cra

ALIGNMENTS

RESULT 1	AX350504	20 bp	DNA	linear	PAT 06-FEB-2002
LOCUS	AX350504	Sequence 16 from Patent WO0179561.			
DEFINITION	AX350504				
ACCESSION	AX350504.1	GI:18616100			
VERSION	AX350504.1				
KEYWORDS					
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.				
REFERENCE	Liggett, S.B. and Small, K.M.				
AUTHORS	Alpha-2 adrenergic receptor polymorphisms				
TITLE	Patent: WO 0179561-A 16 25-OCT-2001;				
JOURNAL					

FEATURES
source
liggett, Stephen B. (US) ; Small, Kersten M. (US)
Location/Qualifiers
1..20
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"

BASE COUNT
10 a 6 c 3 g 1 t

Query Match
Best Local Similarity 100.0%; Score 20; DB 6; Length 20;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY
1 AAAAAGCCCATGACACAG 20
1 AAAAAGCCCATGACACAG 20

Db
1 AAAAAGCCCATGACACAG 20

RESULT 2
HUMA2C2/c 885 bp DNA linear PRI 06-MAR-1995
LOCUS
DEFINITION Human alpha-2 adrenergic receptor (ADRA2C) gene, partial cds.
ACCESSION M38742
VERSION M38742.1 GI:1177867
KEYWORDS alpha-2 adrenergic receptor.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 885)
Chang, A.C., Ho, T.F. and Chang, N.C.
In vitro amplification by polymerase chain reaction of a partial
gene encoding the third subtype of alpha-2 adrenergic receptor in
humans
Biochem. Biophys. Res. Commun. 172 (2), 817-823 (1990)
JOURNAL MEDLINE
PUBMED 2173582
COMMENT Original source text: Human adult neuroblastoma DNA, clone PCRA2.
Draft entry and computer-readable sequence for [unpublished (1990)]
kindly submitted
by A.C.Chang, 20-SEP-1990.
Institute of Neuroscience
155, Sect II, Li-Noon St.
Taipei, Taiwan, 11221 ROC.
Location/Qualifiers
1..885
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/map="4p16.3-p15"
/clone="PCRA2"
/cell_line="neuroblastoma SK-N-SH"
/cell_type="neuroblastoma"
/tissue_type="neural"
/dev_stage="adult"
1..885
/gene="ADRA2C"
1..885
/partial
/gene="ADRA2C"
/codon_start=1
/product="alpha-2-adrenergic receptor"
/protein_id="AAA62823.1"
/db_xref="GI:177868"
/db_xref="GDB:G00-120-540"
/translation="PCTSTVHLCALISDRWANSRALEFNSKTRPRIKITITLWV
LAAVLSPLLYKDGQDPQGRGPOCKINQEWYILASISGFPAPCLIMLVYRTY
LIAKSNRGRPRAGKGGQGGSGKOPRPHGALASAKLPALASVASAEVNGHSKSTG
KKEEGTPEDTGTALPSPMALPNSGOGKEGVCAPEDEAEEREEEREEERCEP
QAVPSPACSGPPLQPGQSRVLTNGQVLGRGVAIGGQWRRRAOLTRERKFT
FVLAVYIGVFCWCPFRFF"

BASE COUNT
152 a 285 c 285 g 163 t

Query Match
Best Local Similarity 100.0%; Score 20; DB 9; Length 885;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY
1 AAAAAGCCCATGACACAG 20
1 AAAAAGCCCATGACACAG 839

Db
1 AAAAAGCCCATGACACAG 839

RESULT 3
AX350490/c 1344 bp DNA linear PAT 06-FEB-2002
LOCUS
DEFINITION Sequence 2 from Patent WO0179561.
ACCESSION AX350490
VERSION AX350490.1 GI:18616092
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1
Liggett, S.B. and Small, K.M.
Alpha-2 adrenergic receptor polymorphisms
Patent: WO 0179561-A 2 25-OCT-2001;
Liggett, Stephen B. (US) ; Small, Kersten M. (US)
Location/Qualifiers
1..1344
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"

BASE COUNT
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Query Match
Best Local Similarity 100.0%; Score 20; DB 6; Length 1344;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY
1 AAAAAGCCCATGACACAG 20
1 AAAAAGCCCATGACACAG 1112

Db
1 AAAAAGCCCATGACACAG 1112

RESULT 4
AF316895/c 1344 bp DNA linear PRI 13-FEB-2001
LOCUS
DEFINITION Homo sapiens alpha 2B adrenergic receptor (ADRA2B) gene, complete
cds.
ACCESSION AF316895
VERSION AF316895.1 GI:12698669
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 1344)
Small, K.M., Brown, K.M., Forbes, S.L. and Liggett, S.B.
Polymorphic deletion of three intracellular acidic residues of the
alpha 2B-adrenergic receptor decreases G protein-coupled receptor
kinase-mediated phosphorylation and desensitization
J Biol Chem. 276 (7), 4917-4922 (2001)
JOURNAL MEDLINE
PUBMED 11056163
REFERENCE 2 (bases 1 to 1344)
Small, K.M., Brown, K.M., Forbes, S.L. and Liggett, S.B.
Direct Submission
Submitted (26-OCT-2000) Internal Medicine, University of
Cincinnati, 231 Bethesda Ave, Cincinnati, OH 45267, USA
Cincinnati
Location/Qualifiers
1..1344
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"

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 /gene="ADRA2B"
 mRNA <1..>1344
 /gene="ADRA2B"
 /product="alpha 2B adrenergic receptor"
 1..1344
 /gene="ADRA2B"
 /note="G-protein coupled receptor"

/codon_start=1
 /product="alpha 2B adrenergic receptor"
 /protein_id="AAK01635.1"
 /db_xref="GI:12698670"

variation
 /gene="ADRA2B"
 /note="compared to wild type sequence presented in GenBank
 accession Number AF005900; polymorphic sequence lacks
 three glu residues at this location"
 /frequency="Caucasians 0.31; African-Americans 0.12"
 /replace="gaagagagag"
 891..892

BASE COUNT 220 a 458 c 400 g 266 t
 ORIGIN

Query Match 100.0%; Score 20; DB 9; Length 1344;
 Best Local Similarity 100.0%; Pred. No. 9.5; Mismatches 0; Indels 0; Gaps 0;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAAAAGCCCAATGACCACAG 20
 Db 1131 AAAAAGCCCAATGACCACAG 1112

RESULT 5
 AX350489/c 1353 bp DNA linear PAT 06-FEB-2002
 LOCUS AX350489
 DEFINITION Sequence 1 from Patent WO0119561.
 ACCESSION AX350489
 VERSION AX350489.1 GI:18616091
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1
 Liggett, S.B. and Small, K.M.
 Alpha-2 adrenergic receptor polymorphisms
 Patent: WO 0179561-A 1 25-OCT-2001;
 JOURNAL Liggett, Stephen B. (US) ; Small, Kersten M. (US)
 FEATURES
 source 1..1353
 /organism="Homo sapiens"
 /mol_type="genomic DNA"
 /db_xref="taxon:9606"

BASE COUNT 224 a 458 c 405 g 266 t
 ORIGIN

Query Match 100.0%; Score 20; DB 6; Length 1353;
 Best Local Similarity 100.0%; Pred. No. 9.5; Mismatches 0; Indels 0; Gaps 0;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAAAAGCCCAATGACCACAG 20
 Db 1140 AAAAAGCCCAATGACCACAG 1121

RESULT 6
 AR270618/c 2072 bp DNA linear PAT 10-APR-2003
 LOCUS AR270618
 DEFINITION Sequence 1181 from patent US 6500938.
 ACCESSION AR270618
 VERSION AR270618.1 GI:29701852
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.

REFERENCE 1 (bases 1 to 2072)
 Au-Young, J. and Seilhamer, J.J.
 Composition for the detection of signaling pathway gene expression
 Patent: US 6500938-A 1181 31-DEC-2002;
 FEATURES
 source 1..2072
 /organism="unknown"

BASE COUNT 316 a 705 c 660 g 391 t
 ORIGIN

Query Match 100.0%; Score 20; DB 6; Length 2072;
 Best Local Similarity 100.0%; Pred. No. 9.9; Mismatches 0; Indels 0; Gaps 0;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAAAAGCCCAATGACCACAG 20
 Db 1552 AAAAAGCCCAATGACCACAG 1533

RESULT 7
 HUMADRA2RA/c 2072 bp DNA linear PRI 30-OCT-1994
 LOCUS HUMADRA2RA
 DEFINITION Human alpha-2-adrenergic receptor (alpha-2 c2) gene, complete cds.
 ACCESSION M34041
 VERSION M34041.1 GI:178197
 KEYWORDS alpha-2-adrenergic receptor; plasma membrane protein;
 receptor-coupled G protein.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 2072)
 Lomasney, J.W., Lorenz, W., Allen, L.F., King, K., Regan, J.W.,
 Yang-Feng, T.L., Caron, M.G. and Lefkowitz, R.J.
 Expansion of the alpha 2-adrenergic receptor family: cloning and
 characterization of a human alpha 2-adrenergic receptor subtype,
 the gene for which is located on chromosome 2
 Proc. Natl. Acad. Sci. U.S.A. 87 (13), 5094-5098 (1990)

JOURNAL 90311349
 MEDLINE 2164221
 COMMENT Original source text: Human placenta DNA, clone alpha-2 C2.
 Draft entry and computer-readable sequence for (1) kindly submitted
 by J.W. Lomasney, 03-MAY-1990, for release after publication.

FEATURES
 source 1..2072
 /organism="Homo sapiens"
 /mol_type="genomic DNA"
 /db_xref="taxon:9606"

gene 413..1765
 /gene="ADRA2B"
 /note="alpha-2-adrenergic receptor (alpha-2 C2) old gene
 name 'ADRA2RL1'"
 /codon_start=1
 /protein_id="AAAS1666.1"
 /db_xref="GI:178198"

CDS

1 AAAAAGCCCAATGACCACAG 20
 1140 AAAAAGCCCAATGACCACAG 1121

KOPRPHGAGALASAKI.PALASVARSAREVNGHSTGKEGETPEDTGTAL.PPSMA
LPSGCGKRGVCGASPEDAREEEEECECPQAVPSAPACSPPLQOQGR
VLATLKGQVLIGRGVATIGCGWRRAHHTREKRTFLAVVIGVFLCMFPFFSYS
LGAICPRKCVPHGLFQFFFWIGYCNSLNPVITYITIFNDPRARILICRPMQTAM

BASE COUNT 316 a 705 c 660 g 391 t
ORIGIN Chromosome 2.

Query Match 100.0%; Score 20; DB 9; Length 2072;
Best Local Similarity 100.0%; Pred. No. 9.9; 0; Indels 0; Gaps 0;
Matches 20; Conservative 0; Mismatches 0;

Qy 1 AAAAAGCCCAATGACACAG 20
Db 1552 AAAAAGCCCAATGACACAG 1533

RESULT 8
AX548756/c
LOCUS Sequence 41 from Patent WO02061087.
DEFINITION AX548756 DNA linear PAT 26-NOV-2002
ACCESSION AX548756
VERSION AX548756.1 GI:25813686
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
AUTHORS 1 Burner, G.C., Roush, C.L. and Brown, J.P.
TITLE Antigenic peptides, such as for G protein-coupled receptors
JOURNAL (GPCRs), antipeptides thereto, and systems for identifying such
LIFEspan Biosciences, Inc. (US)
PATENT: WO 02061087-A 41 08-AUG-2002;
LOCATION/Qualifiers
1..3274
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"

BASE COUNT 587 a 967 g 741 t
ORIGIN

Query Match 100.0%; Score 20; DB 6; Length 3274;
Best Local Similarity 100.0%; Pred. No. 10; 0; Indels 0; Gaps 0;
Matches 20; Conservative 0; Mismatches 0;

Qy 1 AAAAAGCCCAATGACACAG 20
Db 1140 AAAAAGCCCAATGACACAG 1121

RESULT 9
AF005900/c
LOCUS Homo sapiens alpha2B-adrenergic receptor (alpha2C2AR) gene,
DEFINITION AF005900 complete cds.
ACCESSION AF005900
VERSION AF005900.1 GI:2245627
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
AUTHORS 1 (bases 1 to 9842) Bouloumie, A., Devedjian, J.C. and Paris, H.
TITLE Alpha2C2-adrenergic receptor gene
JOURNAL Unpublished
AUTHORS 2 (bases 1 to 9842) Bouloumie, A., Devedjian, J.C. and Paris, H.
TITLE Direct Submission
JOURNAL Submitted (29-MAY-1997) INSERM Unit 317, Institut Louis Bugnard,
CHU Rangueil, Toulouse 31403, France

FEATURES
source Location/Qualifiers
1..9842
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="2"
/clone_lib="brain fetal genomic library"
5398..6750
/gene="alpha2C2AR"
/note="alpha2C2 adrenergic receptor gene"
5398..6750
/gene="alpha2C2AR"
/note="adrenergic receptor"
/product="alpha2B-adrenergic receptor"
/protein_id="PAB62558.1"
/db_xref="GI:2245628"
/translation="MDHDPYSQATRAATATPILFTFGNALVILAVTSRLR
APQNLPLVSLAADIIVATLIPFSLABELLGTWYRRRTCEVYLAIDVLFCGSSIVH
LCAISLDYVWVSRALRYNSKRTPRKICILVTLVILAKRSNRKPRKAGCGQES
RPOCKLNOEAMVILASSIGSFAPCHIMLVIRYLAKRSNRKPRKAGCGQES
KOPRPHGAGALASAKI.PALASVARSAREVNGHSTGKEGETPEDTGTAL.PPSMA
LPSGCGKRGVCGASPEDAREEEEECECPQAVPSAPACSPPLQOQGR
VLATLKGQVLIGRGVATIGCGWRRAHHTREKRTFLAVVIGVFLCMFPFFSYS
LGAICPRKCVPHGLFQFFFWIGYCNSLNPVITYITIFNDPRARILICRPMQTAM

BASE COUNT 1870 a 2747 c 3225 g 1998 t 2 others
ORIGIN polyA_signal 8649..8654

Query Match 100.0%; Score 20; DB 9; Length 9842;
Best Local Similarity 100.0%; Pred. No. 12; 0; Indels 0; Gaps 0;
Matches 20; Conservative 0; Mismatches 0;

Qy 1 AAAAAGCCCAATGACACAG 20
Db 6537 AAAAAGCCCAATGACACAG 6518

RESULT 10
AC092603
LOCUS Homo sapiens BAC clone RPL1-139J6 from 2, complete sequence.
DEFINITION AC092603 AC073396
VERSION AC092603.2 GI:16303539
KEYWORDS HTG.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
AUTHORS 1 (bases 1 to 22842) Sultston, J.E. and Waterston, R.
TITLE Toward a complete human genome sequence
JOURNAL Genome Res. 8 (11), 1097-1108 (1998)
MEDLINE 99063792
PUBMED 9847074

REFERENCE
AUTHORS 2 (bases 1 to 22842) Martinka, S., Abbott, A., Hawkins, M., Elliott, G. and Doeber, A.
TITLE The sequence of Homo sapiens BAC clone RPL1-139J6
JOURNAL Unpublished (2001)
AUTHORS 3 (bases 1 to 22842) Waterston, R.H.
TITLE Direct Submission
JOURNAL Submitted (19-JUL-2001) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
4 (bases 1 to 22842) Waterston, R.H.
TITLE Direct Submission
JOURNAL Submitted (20-OCT-2001) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
5 (bases 1 to 22842)

AUTHORS
TITLE
JOURNAL
Waterston, R.H.
Direct Submission
Submitted (23-OCT-2001) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
6 (bases 1 to 22842)
Waterston, R.
REFERENCE
TITLE
JOURNAL
Submitted (01-MAR-2002) Department of Genetics, Washington
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
On Oct 20, 2001 this sequence version replaced gi:14916188.
COMMENT

Center: Washington University Genome Sequencing Center
Center code: WUGSC
Web site: <http://genome.wustl.edu/gsc>
Contact: sapiens@wustl.wustl.edu

Summary Statistics
Center project name: H_NH0139006
Drafting Center: WIBR

NOTICE: This sequence may not represent the entire insert of this
clone. It may be shorter because we only sequence overlapping
clone sections once, or longer because we provide a small overlap
between neighboring data submissions.

This sequence was finished as follows unless otherwise noted:
all regions were double stranded, sequenced with an alternate
chemistry, or covered by high quality data (i.e., phred quality >=
30); an attempt was made to resolve all sequencing problems, such
as compressions and repeats; all regions were covered by sequence
from more than one subclone; and the assembly was confirmed by
restriction digest.

MAPPING INFORMATION:
Mapping information for this clone was provided by Dr. John D.
McPherson, Department of Genetics, Washington University, St. Louis
MO. For additional information about the map position of this
sequence, see <http://genome.wustl.edu/gsc>

SOURCE INFORMATION:
The RPCT-11 human BAC library was made from the blood of one male
donor, as described by Osoegawa, K., Moon, P.Y., Zhao, B., Frengen, E.,
Tateno, M., Caranese, J.J. and de Jong, P.J. (1998) An improved
approach for construction of bacterial artificial chromosome
libraries. Genomics 51:1-8. The clone may be obtained either from
Research Genetics, Inc. (<http://www.resgen.com>) or Pieter de Jong
and coworkers at <http://www.choil.org>
VECTOR: pBACe3.6

NEIGHBORING SEQUENCE INFORMATION:
The clone sequenced to the left is RP11-401C13, 2000 bp overlap;
the clone sequenced to the right is RP11-574O17, 2000 bp overlap.
Actual end of this clone is at base position 48999 of RP11-574O17.

Polymorphisms have been identified between AC012272 and AC092603.

The sequence of AC073396 has been incorporated into AC092603.

FEATURES
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Location/Qualifiers
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/db_xref="taxon:9606"
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/map="2"
/clone="RP11-139J6"
/clone_11b="RPCT-11"
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repeat_region
1377. .1424
/rpt_family="TG)n"
1424. .1449
/rpt_family="G)n"
repeat_region
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repeat_region
1495. .1665
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1669. .1966
/rpt_family="Alu"
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2812. .2918
/rpt_family="MIR"
repeat_region
3183. .3448
/rpt_family="CT-rich"
repeat_region
5541. .5566
/rpt_family="AT-rich"
repeat_region
5576. .5870
/rpt_family="Alu"
repeat_region
5873. .6183
/rpt_family="Alu"
repeat_region
6195. .6301
/rpt_family="MIR"
repeat_region
6627. .6733
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repeat_region
7278. .7415
/rpt_family="MIR"
repeat_region
7698. .7723
/rpt_family="(GGCTG)n"
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8140. .8218
/rpt_family="G-rich"
repeat_region
8863. .8922
/rpt_family="MIR"
repeat_region
9191. .9346
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repeat_region
10172. .10296
/rpt_family="MIR"
repeat_region
10436. .10550
/rpt_family="MIR"
repeat_region
11016. .11169
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repeat_region
11617. .11862
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misc_feature
12062. .12532
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misc_feature
12062. .12257
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misc_feature
12378. .12902
/note="match to EST A1791589 (NID:G5339305) oJ40H05.Y5"
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misc_feature
13072. .13459
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misc_feature
14030. .14244
/note="similar to Homo sapiens EST T39448 (NID:G647179)
YA06A09.r2"
misc_feature
14060. .14247
/note="similar to Homo sapiens EST AL549866
(NID:G12886265) "
misc_feature
14060. .14247
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(NID:G12933576) "
repeat_region
14413. .14439
/rpt_family="(TCC)n"
misc_feature
14762. .14822
/note="similar to Homo sapiens EST AL544609
(NID:G12877089) "
misc_feature
14849. .16413
/note="CPG island (%GC=74.2, o/e=0.90, #CPGs=191) "
misc_feature
14900. .15218
/note="similar to Homo sapiens EST AL544609
(NID:G12877089) "
misc_feature
15084. .15487
/note="similar to Sus scrofa EST AW785035 (NID:G7841811) "
15110. .15648
/note="similar to Rattus norvegicus EST AN916723
(NID:G8082456) "
repeat_region
15747. .15832
/rpt_family="G-rich"
18481. .18596

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repeat_region      /rpt family="L2"
19266..19675
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20027..20223
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20316..20416
repeat_region      /rpt family="L2"
20537..20973
repeat_region      /rpt family="L2"
22057..22471
misc_feature        /note="match to EST AA830781 (NID:g2903880) cc56d01.s1"
22057..22208
misc_feature        /note="match to EST AA836522 (NID:g2910841) cd22d08.s1"
4797 a 7173 c 6248 g 4624 t

BASE COUNT      4797 a 7173 c 6248 g 4624 t

ORIGIN
Query Match      100.0%; Score 20; DB 9; Length 22842;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 AAAAAGCCCAATGACACAG 20
|||||
Db 14200 AAAAAGCCCAATGACACAG 14219

RESULT 11
LOCUS      PVI251176      1168 bp      DNA      linear      MAM 01-JUN-2001
DEFINITION Phoca vitulina partial aar2B gene for alpha adrenergic receptor 2B.
ACCESSION      AJ251176
VERSION      AJ251176.1 GI:11322419
KEYWORDS      aar2B gene; alpha adrenergic receptor 2B.
SOURCE      Phoca vitulina (harbor seal)
ORGANISM      Phoca vitulina
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Pinnipedia; Phocidae; Phoca.

REFERENCE
1      Madsen, O., Scally, M., Donady, C.J., Kao, D.J., DeBry, R.W., Adkins, R.,
Amitine, H.M., Stanhope, M.J., de Jong, W.W. and Springer, M.S.
Parallel adaptive radiations in two major clades of placental
mammals
JOURNAL      Nature 409 (6820), 610-614 (2001)
MEDLINE      21082081
PUBMED      11214318
REFERENCE      2 (bases 1 to 1168)
Madsen, O.
Direct Submission
Submitted (18-NOV-1999) Madsen O., Department of Biochemistry,
University of Nijmegen, P.O. box 9101, 6500 HB Nijmegen,
NETHERLANDS

FEATURES
source
1..1168
/organism="Phoca vitulina"
/mol_type="genomic DNA"
/db_xref="taxon:9720"
1..1168
/gene="aar2B"
<1..>1168
/gene="aar2B"
/codon_start=2
/product="alpha adrenergic receptor 2B"
/protein_id="CAC16696.1"
/db_xref="GI:11322420"
/db_xref="SPTREMBL:O9GL07"
/translation="ATAATTTLLTFTFGNSLVILAVTSTRSLRAPONTFVLSLAA
DILVATLIPFSLANELLGWYFRRTWCEVYALVLFCTSSIVHLCAISLDRTWYAS
RALEVNSKRTPRRIKCIILTVMILAAVSLPLIKYGGPQPGAPQCKLQGEAWYI
LASISGFAPCLIMILVLRILYLAKSRHSGPAKGPGGSGKQPSVPTGTSTK
LPTLASIASEERANGSKPTGEGTDEDTPTPALPSSMALPSSGOGSKGVCAS
PSEBAEEREEERECERPOLPASPASACSPLOPOGSRVILATLRGVLLGRGVGTAS
GGMWRRAQLTRERKRTFVLAIVIGVFLCMFFFFSYSLGALCPQCKVPHGLF"

BASE COUNT      189 a 398 c 351 g 230 t

ORIGIN

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Query Match      92.0%; Score 18.4; DB 4; Length 1168;
Best Local Similarity 95.0%; Pred. No. 72;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 AAAAAGCCCAATGACACAG 20
|||||
Db 1084 AAAAAGCCCAATGACACAG 1065

RESULT 12
LOCUS      SSC251177      1174 bp      DNA      linear      MAM 01-JUN-2001
DEFINITION Sus scrofa partial aar2B gene for alpha adrenergic receptor 2B.
ACCESSION      AJ251177
VERSION      AJ251177.1 GI:11322421
KEYWORDS      aar2B gene; alpha adrenergic receptor 2B.
SOURCE      Sus scrofa (pig)
ORGANISM      Sus scrofa
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.

REFERENCE
1      Madsen, O., Scally, M., Donady, C.J., Kao, D.J., DeBry, R.W., Adkins, R.,
Amitine, H.M., Stanhope, M.J., de Jong, W.W. and Springer, M.S.
Parallel adaptive radiations in two major clades of placental
mammals
JOURNAL      Nature 409 (6820), 610-614 (2001)
MEDLINE      21082081
PUBMED      11214318
REFERENCE      2 (bases 1 to 1174)
Madsen, O.
Direct Submission
Submitted (18-NOV-1999) Madsen O., Department of Biochemistry,
University of Nijmegen, P.O. box 9101, 6500 HB Nijmegen,
NETHERLANDS

FEATURES
source
1..1174
/organism="Sus scrofa"
/mol_type="genomic DNA"
/db_xref="taxon:9823"
1..1174
/gene="aar2B"
<1..>1174
/gene="aar2B"
/codon_start=2
/product="alpha adrenergic receptor 2B"
/protein_id="CAC16697.1"
/db_xref="GI:11322422"
/db_xref="SPTREMBL:O9GL06"
/translation="ATAATTTLLTFTFGNSLVILAVTSTRSLRAPONTFVLSLAA
DILVATLIPFSLANELLGWYFRRTWCEVYALVLFCTSSIVHLCAISLDRTWYAS
RALEVNSKRTPRRIKCIILTVMILAAVSLPLIKYGGPQPGAPQCKLQGEAWYI
LASISGFAPCLIMILVLRILYLAKSRHSGPAKGPGGSGKQPSVPTGTSTK
LPTLASIASEERANGSKPTGEGTDEDTPTPALPSSMALPSSGOGSKGVCAS
PSEBAEEREEERECERPOLPASPASACSPLOPOGSRVILATLRGVLLGRGVGTAS
GGMWRRAQLTRERKRTFVLAIVIGVFLCMFFFFSYSLGALCPQCKVPHGLF"

BASE COUNT      196 a 376 c 346 g 256 t

ORIGIN
Query Match      92.0%; Score 18.4; DB 4; Length 1174;
Best Local Similarity 95.0%; Pred. No. 72;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 AAAAAGCCCAATGACACAG 20
|||||
Db 1090 AAAAAGCCCAATGACACAG 1071

RESULT 13
LOCUS      ASP427259      1185 bp      DNA      linear      ROD 25-OCT-2002
DEFINITION Anomalurus sp. partial A2AB gene for alpha 2B adrenergic receptor,
exon 1.

```

FEATURES	source	Location/Qualifiers
gene		1..1185
CDS		/organism="Anomalurus sp."
		/mol_type="genomic DNA"
		/db_xref="taxon:101665"
		1..1185
		/gene="A2AB"
		<1..>1185
		/gene="A2AB"
		/codon_start=1
		/product="alpha 2B adrenergic receptor"
		/protein_id="CAD30297.1"
		/db_xref="GI:21655550"
		/translation="ATAATTTFLTFETFGNAVTILAVTSHSRAPONTFLVSLAAN DIVATITLIPPSLANELLGTYFSTMCVETLADVLFTSSIVHLCAISIDRYWAVS PALEYSNKRTPRRIRKILILWLIAVAISLPLLYKDDQGPGRQCKLNDGAWYI LASIGSFAPACILMILVYLRIVIAKSNRGRPTNGRPGCGESKQFPVPGCAPAS AKVTLSPLSSAGCANGHPKRPGEKGEETPDGPALPSSWALPNSSQGGKGA CGAAEEEAEEEEEEEBECBPQAVPVSPASVCSOPLQDQGSRLVATLRGVLGR HVCNAGCGWMRRRQLSREKRTVLAVIGVFLVCMPPFFFSISLCAICPHCKVPRH GLF"
exon		<1..>1185
		/gene="A2AB"
		/number=1
BASE COUNT	202 a 391 c 344 g 247 t	1 others
ORIGIN		
Query Match	92.0%; Score 18.4; DB 10; Length 1185;	
Best Local Similarity	95.0%; Pred. No. 72;	
Matches	19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;	
QY	1 AAAAAAGCCATGACACAG 20	
Db	1101 AAGAGCGCATGACACAG 1082	
RESULT 14		
AL840630		
LOCUS	AL840630 149169 bp DNA linear VRT 24-MAY-2003	
DEFINITION	Zebrafish DNA sequence from clone CH211-279L11 in linkage group 17,	
ACCESSION	AL840630	
VERSION	AL840630	
KEYWORDS	Complete sequence.	
SOURCE	AL840630.15 GI:31071445	
ORGANISM	HTG.	
	Danio rerio (zebrafish)	
	Danio rerio	
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
	Actinopterygii; Neopterygii; Teleostei; Ostariophysi;	
	Cypriniformes; Cyprinidae; Danio.	
REFERENCE	1 (bases 1 to 149169)	

AUTHORS Direct Submission
 TITLE
 JOURNAL Submitted (24-MAY-2003) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: zfish-help@sanger.ac.uk
 On May 23, 2003 this sequence version replaced gi:30722485.
 COMMENT

 Center: Wellcome Trust Sanger Institute
 Center code: SC
 Web site: http://www.sanger.ac.uk
 Contact: zfish-help@sanger.ac.uk

 During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.
 This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30) ; an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest, except on the rare occasion of the clone being a YAC.
 The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em: EMBL; Sw: SWISSPROT; Tr: TREMBL; Wp: WORMPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/projects/C_elegans/wormpep
 Repeat names beginning 'Dr' were identified by the Recon repeat discovery system (Zhifeng Bao and Sean Eddy, submitted), and those beginning 'dtr' were identified by Rick Waterman (Stephen Johnson lab, WashU). For further information see http://www.sanger.ac.uk/Projects/D_rexio/fishmask.shtml
 CH211-279L11 is from a CHOR1-211 BAC library
 VECTOR: PTARBAC2.1.
 Location/Qualifiers
 1. 149169
 /organism="Danio rerio"
 /mol_type="genomic DNA"
 /db_xref="taxon:7955"
 /clone="CH211-279L11"
 /clone_lib="CHOR1-211"
 47889 a 26273 c 26492 g 48515 t
 BASE COUNT
 ORIGIN
 Query Match 92.0%; Score 18.4; DB 5; Length 149169;
 Best Local Similarity 95.0%; Pval. No. 1.2e+02;
 Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 AAAAAGCCCATGACCCACAG 20
 |||||
 Db 21021 AAAAAGCCCATGACCCACAG 21040
 RESULT 15
 BXS10991/c BXS10991 171406 bp DNA linear HTG 22-MAY-2003
 LOCUS
 DEFINITION Danio rerio clone RP71-44C4, *** SEQUENCING IN PROGRESS ***, 8
 unorderd pieces.
 ACCESSION BXS10991
 VERSION BXS10991.3 GI:31071389
 KEYWORDS HTG; HTGS PHASRI.
 SOURCE
 ORGANISM Danio rerio (zebrafish)
 Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Danio.
 1 (bases 1 to 171406)
 REFERENCE
 AUTHORS Sims, S.
 TITLE Direct Submission

JOURNAL Submitted (21-MAY-2003) Wellcome Trust Sanger Institute, Hinxton,
Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
zfish-help@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
COMMENT On May 23, 2003 this sequence version replaced gi:30962299.

----- Genome Center
Center: Wellcome Trust Sanger Institute
Center code: SC
Web site: http://www.sanger.ac.uk
Contact: zfish-help@sanger.ac.uk
----- Project Information
Center project name: b244C4
----- Summary Statistics
Assembly program: XGAP4; version 4.5
Chemistry: Dye-terminator; 100% of reads
Consensus quality: 167404 bases at least Q40
Consensus quality: 168324 bases at least Q30
Consensus quality: 169018 bases at least Q20
Insert size: 170706; sum-of-contigs
Insert size: 169513; 3.5% error; agarose-fp
Quality coverage: 7.49x in Q20 bases; sum-of-contigs Quality
coverage: 7.55x in Q20 bases; agarose-fp

* NOTE: This is a 'working draft' sequence. It currently
* consists of 8 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

1 56569: contig of 56569 bp in length
* 56570 56669: gap of 100 bp
* 56670 62067: contig of 5398 bp in length
* 62068 62167: gap of 100 bp
* 62168 88720: contig of 26553 bp in length
* 88721 88820: gap of 100 bp
* 88821 134708: contig of 45888 bp in length
* 134709 134808: gap of 100 bp
* 134809 142476: contig of 7668 bp in length
* 142477 142576: gap of 100 bp
* 142577 154106: contig of 11530 bp in length
* 154107 154206: gap of 100 bp
* 154207 164114: contig of 9908 bp in length
* 164115 164214: gap of 100 bp
* 164215 171406: contig of 7192 bp in length.

FEATURES
Source
1..171406
/organism="Danio rerio"
/mol_type="genomic DNA"
/db_xref="taxon:7955"
/clone="RP71-44C4"
/clone_1lb="RPCT-71"

misc_feature
1..56569
/note="assembly_fragment:01943
fragment_chain:1
clone_end:T7
vector_side:left"
56670..62067
/note="assembly_fragment:00525
fragment_chain:1"
62168..88720
/note="assembly_fragment:02082
fragment_chain:1"
88821..134708
/note="assembly_fragment:01880
fragment_chain:1"
134809..142476
/note="assembly_fragment:01032
fragment_chain:1"
142577..154106
/note="assembly_fragment:01420
fragment_chain:1"
154207..164114

/note="assembly_fragment:00067
fragment_chain:1"
164215..171406
/note="assembly_fragment:00689
fragment_chain:1
clone_end:SP6
vector_side:right"

BASE COUNT 57035 a 29367 c 29252 g 55051 t 701 others
ORIGIN

Query Match 92.0%; Score 18.4; DB 2; Length 171406;
Best Local Similarity 95.0%; Pred.No. 1.2e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AAAAAGCCATGACCCACG 20
Db 33134 AAAAAGCCATGACCCACG 33115

Search completed: February 12, 2004, 04:41:51
Job time : 589.854 secs

XX
DR 20-OCT-2000; 2000WO-FI00913.
XX 22-OCT-1999; 99US-0422985.
XX (JUVV-) JUVANTIA PHARMA LTD OY.
XX Snajir A, Heinoonen P, Alhopuro P, Karvonen M, Koulu M, Pesonen U;
XX Scheinin M, Salonen JT, Tuomala T, Lakkia TA, Myllynen K;
XX Salonen R, Kautanen U, Valkonen V;
XX WPI; 2001-300318/31.
XX P-PSDB; AAE00989.
XX
XX The invention relates to genotyping an alpha-2B, 2A, or 2C adrenergic
XX receptor gene (I)-(III) by detecting a polymorphic site, comprising:
XX (a) obtaining a sample having a polynucleotide encoding an alpha-2B,
XX alpha-2A or alpha-2C or fragment or complement of; and
XX (b) detecting a polymorphic site comprising nucleotide positions 901-909
XX of (I), a site comprising cytosine or guanine at position 753 of (IIV)
XX or a site comprising (A) (999GCG999GCG) or (B) (999GCGCTAG) at
XX positions 961-972 of (III). The method may be used for genotyping an
XX alpha-2B, alpha-2A or alpha-2C receptor gene and further used to determine
XX whether an individual is at increased risk of developing a disease
XX associated with alpha-2B, alpha-2A or alpha-2C, comprising detecting a
XX polymorphic site which correlate to disease selected from cardiovascular
XX disease, central nervous system disease and combinations of these. In
XX addition, the technique may be used to predict an individual's response
XX to an alpha-2B, alpha-2A, or alpha-2C agonist (e.g. epinephrine, BHT933 and
XX norepinephrine, clonidine, oxymetazoline, guanabenz, UK14304, BHT933 and
XX combinations of these) or antagonist (e.g. yohimbine, prazosin, AKC 239,
XX rauwolfine, idazoxan, tolazoline, phentolamine and combinations of
XX these) by detecting the polymorphic site and correlating the site to a
XX predetermined response (where the response is correlated to adenylyl
XX cyclase, MAP kinase activity, phosphorylation or inositol phosphate
XX levels). The present sequence is that of a human alpha-2BAR PCR primer,
XX useful for the genotyping methods of the invention.
XX
SQ Sequence 20 BP; 10 A; 6 C; 3 G; 1 T; 0 other;
Query Match 100.0%; Score 20; DB 23; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.6; Indels 0; Gaps 0;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AAAAAGCCCATGACACAG 20
DB 1 AAAAAGCCCATGACACAG 20
RESULT 2
AADD04761/c
ID AADD04761 standard; DNA; 1344 BP.
XX
AC AADD04761;
XX
DT 04-JUL-2001 (first entry)
XX
DE Human alpha2B-adrenoceptor (alpha2B-AR) variant gene.
XX
XX Human; cardiact; gene therapy; alpha2B-adrenoceptor; alpha2B-AR;
XX glutamic acid repeat; intracellular loop; chromosome 2; catecholamine;
XX norepinephrine; epinephrine; therapy; vascular contraction; variant;
XX coronary artery; coronary heart disease; CHD; chronic angina pectoris;
XX acute myocardial infarction; AMI; Prinzmetal's variant; ds.
XX
OS Homo sapiens.
XX
XX Key Location/Qualifiers
XX CDS 1..1344
XX FT /*tag= a
XX FT /product= "Human alpha2B-adrenoceptor (alpha2B-AR)"
XX FT variant protein"
XX
XX WO200129082-A1.
XX
XX 26-APR-2001.

PF 20-OCT-2000; 2000WO-FI00913.
XX 22-OCT-1999; 99US-0422985.
XX (JUVV-) JUVANTIA PHARMA LTD OY.
XX Snajir A, Heinoonen P, Alhopuro P, Karvonen M, Koulu M, Pesonen U;
XX Scheinin M, Salonen JT, Tuomala T, Lakkia TA, Myllynen K;
XX Salonen R, Kautanen U, Valkonen V;
XX WPI; 2001-300318/31.
XX P-PSDB; AAE00989.
XX
XX The present sequence is a gene encoding human alpha2B-adrenoceptor
XX (alpha2B-AR) variant protein. Alpha2B-AR has a glutamic acid repeat
XX element (amino acids 298-309) of 12 glutamates, in an acidic stretch of
XX 18 amino acids (amino acids 294-311), located in the third intracellular
XX loop of the receptor polypeptide. The variant is obtained by deletion of
XX three glutamates from the Glu repeat (amino acids 307-309). Alpha2B-AR
XX gene is located on chromosome 2. Alpha2-AR mediate many of the
XX physiological effects of the catecholamines, norepinephrine and
XX epinephrine. An antagonist of alpha2B-adrenoceptor is useful for treating
XX a mammal suffering from vascular contraction of coronary arteries and a
XX disease involving vascular contraction of coronary arteries which is
XX clinically expressed as coronary heart disease (CHD), unstable chronic
XX angina pectoris which is clinically expressed as Prinzmetal's variant
XX form of acute myocardial infarction (AMI). Alpha2B-AR gene is used in
XX gene therapy.
XX
SQ Sequence 1344 BP; 219 A; 459 C; 400 G; 266 T; 0 other;
Query Match 100.0%; Score 20; DB 22; Length 1344;
Best Local Similarity 100.0%; Pred. No. 5.7; Indels 0; Gaps 0;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AAAAAGCCCATGACACAG 20
DB 1131 AAAAAGCCCATGACACAG 1112
RESULT 3
AAI99906/c
ID AAI99906 standard; DNA; 1344 BP.
XX
AC AAI99906;
XX
DT 18-FEB-2002 (first entry)
XX
DE Human alpha-2BAR third intracellular loop variant encoding DNA.
XX
XX Human; genotyping; alpha-2B; alpha-2A; alpha-2C; adrenergic receptor;
XX polymorphic site; allelic variant; cardiovascular disease;
XX central nervous system disease; adenylyl cyclase; MAP kinase activity;
XX phosphorylation; inositol phosphate; alpha-2BAR; chromosome 2; ds.
XX
OS Homo sapiens.
XX
XX Key Location/Qualifiers
XX CDS 1..1344
XX FT /*tag= a
XX FT /product= "alpha-2BAR"
XX FT /note= "sequence is deleted for a 9 nucleotide
XX of the wildtype alpha-2BAR protein (AAI99905)"
XX
XX WO200179561-A2.

```

XX 25-OCT-2001.
PD 17-APR-2001; 2001WO-US12575.
XX
XX 17-APR-2001; 2000US-0551744.
XX 10-AUG-2000; 2000US-0636259.
XX 19-OCT-2000; 2000US-0692077.
XX
XX (LIGGETT) LIGGETT S B.
XX (SMALL) SMALL K M.
XX
XX Liggett SB, Small KM;
XX
XX WPI; 2001-611728/70.
XX P-PSDB; AAM52118.
XX
XX Genotyping an alpha-2B, 2A, or 2C adrenergic receptor gene useful for
XX determining whether an individual is at increased risk of developing a
XX disease associated with the corresponding receptor comprises detecting
XX a polymorphic site -
XX
XX Claim 5; Page 144-145; 163pp; English.
XX
XX The invention relates to genotyping an alpha-2B, 2A, or 2C adrenergic
XX receptor gene (I)-(III) by detecting a polymorphic site, comprising:
XX (a) obtaining a sample having a polynucleotide encoding an alpha-2B,
XX alpha2A or alpha2C or fragment or complement of; and
XX (b) detecting a polymorphic site comprising nucleotide positions 901-909
XX of (I), a site comprising cytosine or guanine at position 753 of (IIIV)
XX or a site comprising (A) (GGGCGGCGGCG) or (B) (GGGCGGCGTGA) at
XX positions 961-972 of (III). The method may be used for genotyping an
XX alpha2B, alpha2A or alpha2C receptor gene and further used to determine
XX whether an individual is at increased risk of developing a disease
XX associated with alpha2B, alpha2A or alpha2C, comprising detecting a
XX polymorphic site which correlate to disease selected from cardiovascular
XX disease, central nervous system disease and combinations of these. In
XX addition, the technique may be used to predict an individual's response
XX to an alpha2B, alpha2A, or alpha2C agonist (e.g. epinephrine,
XX norepinephrine, clonidine, oxymetazoline, guanabenz, UK14304, BHT933 and
XX combinations of these) or antagonist (e.g. yohimbine, prazosin, ARC 239,
XX rauwolficine, idazoxan, tolazoline, phenoltamine and combinations of
XX these) by detecting the polymorphic site and correlating the site to a
XX predetermined response (where the response is correlated to adenylyl
XX cyclase, MAP kinase activity, phosphorylation or inositol phosphate
XX levels). The present sequence is that of the third intracellular loop of
XX the human alpha-2BAR variant, the sequence is deleted for a 9 nucleotide
XX polymorphic site found at nucleotides 901-909 of the wildtype gene
XX (AA199905).
XX
XX Sequence 1344 BP; 220 A; 458 C; 400 G; 266 T; 0 other;
XX
XX Query Match 100.0%; Score 20; DB 23; Length 1344;
XX Best Local Similarity 100.0%; Pred. No. 5.7;
XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 AAAAAGCCCAATGACCACAG 20
XX |||||||||||||||||||
XX 1131 AAAAAGCCCAATGACCACAG 1112
XX
XX RESULT 4
XX AAD44388/C
XX ID AAD44388 standard; DNA; 1344 BP.
XX
XX AAD44388;
XX
XX 13-DEC-2002 (first entry)
XX
XX Human alpha-2B-adrenoceptor variant DNA.
XX
XX Human; hypertension; alpha-2B-adrenoceptor; AR; antihypertensive;
XX hypertension; hypotensive; variant; gene; ds.
XX

```

```

XX OS Homo sapiens.
XX OS Synthetic.
XX
XX PH Key Location/Qualifiers
XX CDS 1..1344
XX FT /*tag= a
XX FT /product= "Human alpha-2B-adrenoceptor variant
XX FT protein"
XX
XX PN WO200266617-A1.
XX
XX PD 29-AUG-2002.
XX
XX 13-FEB-2002; 2002WO-FI00113.
XX
XX 20-FEB-2001; 2001FI-0000323.
XX
XX (JURI-) JURILAB LTD OY.
XX
XX Salonen J;
XX
XX WPI; 2002-667063/71.
XX P-PSDB; AAE26633.
XX
XX Detecting a risk of hypertension and targeting treatment in a subject
XX by determining the pattern of alleles encoding a variant
XX alpha-2-adrenoceptor -
XX
XX PS Disclosure; Page 24-26; 35pp; English.
XX
XX The invention relates to a method for detecting a risk of hypertension
XX by determining the pattern of alleles encoding a variant alpha-2B-
XX adrenoceptor (AR) protein. The methods and compositions of the invention
XX are useful for detecting risks and targeting treatment for hypertension.
XX The kit is also useful for selecting for clinical drug trials testing
XX the antihypertensive effect of compounds. The present sequence is human
XX alpha-2B-adrenoceptor variant DNA.
XX
XX Sequence 1344 BP; 219 A; 459 C; 400 G; 266 T; 0 other;
XX
XX Query Match 100.0%; Score 20; DB 24; Length 1344;
XX Best Local Similarity 100.0%; Pred. No. 5.7;
XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 AAAAAGCCCAATGACCACAG 20
XX |||||||||||||||||||
XX 1131 AAAAAGCCCAATGACCACAG 1112
XX
XX RESULT 5
XX AAD04762/C
XX ID AAD04762 standard; DNA; 1353 BP.
XX
XX AAD04762;
XX
XX 04-JUL-2001 (first entry)
XX
XX Human alpha2B-adrenoceptor (alpha2B-AR) gene.
XX
XX Human; cardiant; gene therapy; alpha2B-adrenoceptor; alpha2B-AR;
XX glutamic acid repeat; intracellular loop; chromosome 2; catecholamine;
XX norepinephrine; epinephrine; therapy; vascular contraction;
XX coronary artery; coronary heat disease; CHD; chronic angina pectoris;
XX acute myocardial infarction; AMI; Prinzmetal's variant; ds.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX CDS 1..1353
XX FT /*tag= a
XX FT /product= "Human alpha2B-adrenoceptor (alpha2B-AR)
XX FT protein"
XX

```

XX PN WO200129082-A1.
 XX PD 26-APR-2001.
 XX PF 20-OCT-2000; 2000WO-F100913.
 XX PR 22-OCT-1999; 99US-0422985.
 XX PA (JUVVA-) JUVANTIA PHARMA LTD OY.
 XX PI Snajir A, Heinonen P, Alhopuro P, Karvonen M, Koulu M, Pesonen U,
 PI Scheinin M, Salonen JT, Tuomala T, Lakka TA, Nyssönen K,
 PI Salonen R, Kaunonen J, Valkonen V,
 XX WPI, 2001-300318/31.
 DR P-PSDB; AAE00990.
 XX
 PT New DNA molecule encoding variant specific adrenoceptor protein with
 PT deletion of specific amino acids located in the third intracellular
 PT loop of the polypeptide, for treating vascular contraction of coronary
 PT arteries -
 XX
 PS Disclosure, Page 27-29; 37pp; English.
 XX
 CC The present sequence is a gene encoding human alpha2B-adrenoceptor
 CC (alpha2B-AR) protein. Alpha2B-AR has a glutamic acid repeat element
 CC (amino acids 298-309) of 12 glutamates, in an acidic stretch of 18 amino
 CC acids (amino acids 294-311), located in the third intracellular loop of
 CC the receptor polypeptide. Alpha2B-AR gene is located on chromosome 2.
 CC Alpha2-AR mediate many of the physiological effects of the
 CC catecholamines, norepinephrine and epinephrine. An antagonist of
 CC alpha2B-adrenoceptor is useful for treating a mammal suffering from
 CC vascular contraction of coronary arteries and a disease involving
 CC as coronary heart disease (CHD), unstable chronic angina pectoris which is
 CC clinically expressed as Prinzmetal's variant form or acute myocardial
 CC infarction (AMI). Alpha2B-AR gene is used in gene therapy.
 CC
 SQ Sequence 1353 BP; 223 A; 459 C; 405 G; 266 T; 0 other;
 Query Match 100.0%; Score 20; DB 23; Length 1353;
 Best Local Similarity 100.0%; Pred. No. 5.7;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 AAAAAAGCCAAATGACCAACG 20
 Db 1140 AAAAAAGCCAAATGACCAACG 1121
 RESULT 6
 ID AAI99905 standard; DNA, 1353 BP.
 XX AAI99905;
 AC
 XX 18-FEB-2002 (first entry)
 DT
 XX
 DE Human alpha-2BAR third intracellular loop encoding DNA.
 XX
 KW Human; genotyping; alpha-2B; alpha-2A; alpha-2C; adrenergic receptor;
 KW polymorphic site; allelic variant; cardiovascular disease;
 KW central nervous system disease; adenylyl cyclase; MAP kinase activity;
 KW phosphorylation; inositol phosphate; alpha-2BAR;
 KW GenBank Accession AF009500; chromosome 2; de.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT CDS 1..1353
 FT /tag= a
 FT /product= "alpha-2BAR"
 FT /note= "sequence includes a 9 nucleotide polymorphic site

FT at nucleotides 901-909 absent in the alpha-2BAR
 variant (AAI99906)"
 XX
 XX WO200179561-A2.
 XX PD 25-OCT-2001.
 XX PF 17-APR-2001; 2001WO-US12575.
 XX PR 17-APR-2000; 2000US-0551744.
 XX PR 10-AUG-2000; 2000US-0636259.
 XX PR 19-OCT-2000; 2000US-0692077.
 XX PA (LIGG/) LIGGETT S B.
 XX (SMAL/) SMALL K M.
 XX
 PI Liggett SB, Small KM,
 DR WPI, 2001-611728/70.
 DR P-PSDB; AAM52117.
 XX
 PT Genotyping an alpha-2B, 2A, or 2C adrenergic receptor gene useful for
 PT determining whether an individual is at increased risk of developing a
 PT disease associated with the corresponding receptor comprises detecting a
 PT polymorphic site -
 XX
 PS Claim 4; Page 144; 163pp; English.
 XX
 CC The invention relates to genotyping an alpha-2B, 2A, or 2C adrenergic
 CC receptor gene (I)-(III) by detecting a polymorphic site, comprising:
 CC (a) obtaining a sample having a polynucleotide encoding an alpha-2B,
 CC alpha2A or alpha2C or fragment or complement of; and
 CC (b) detecting a polymorphic site comprising nucleotide positions 901-909
 CC of (I), a site comprising cytosine or guanine at position 753 of (II)
 CC or a site comprising (A) (GGGCGGCGGCG) or (B) (GGGCGGCGTGG) at
 CC positions 961-972 of (III). The method may be used for genotyping an
 CC alpha2B, alpha2A or alpha2C receptor gene, and further used to determine
 CC whether an individual is at increased risk of developing a disease
 CC associated with alpha2B, alpha2A or alpha2C, comprising detecting a
 CC polymorphic site which correlate to disease selected from cardiovascular
 CC disease, central nervous system disease and combinations of these. In
 CC addition, the technique may be used to predict an individual's response
 CC to norepinephrine, clonidine, or alpha2C agonist (e.g. epinephrine,
 CC ramolscine, idazoxan, tolazoline, phenolamine and combinations of
 CC these) by detecting the polymorphic site and correlating the site to a
 CC predetermined response (where the response is correlated to adenylyl
 CC cyclase, MAP kinase activity, phosphorylation or inositol phosphate
 CC levels). The present sequence is that of the third intracellular loop of
 CC the human alpha-2BAR (GenBank Accession AF009500), the sequence includes
 CC a 9 nucleotide polymorphic site at nucleotides 901-909, absent in the
 CC alpha-2BAR variant (AAI99906).
 CC
 SQ Sequence 1353 BP; 224 A; 458 C; 405 G; 266 T; 0 other;
 Query Match 100.0%; Score 20; DB 23; Length 1353;
 Best Local Similarity 100.0%; Pred. No. 5.7;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 AAAAAAGCCAAATGACCAACG 20
 Db 1140 AAAAAAGCCAAATGACCAACG 1121
 RESULT 7
 ID AAD4389/c
 XX AAD4389 standard; DNA, 1353 BP.
 XX AAD4389;
 AC
 XX 13-DEC-2002 (first entry)
 DT
 XX

DE Human alpha-2b-adrenoceptor gene.
 XX
 XX Human; hypertension; alpha-2b-adrenoceptor; AR; antihypertensive;
 KW hypertension; hypotensive; gene; de.
 XX
 OS Homo sapiens.
 XX
 XX Key Location/Qualifiers
 FH 1..1353
 FT CDS /*tag= a
 FT /product= "human alpha-2b-adrenoceptor protein"
 XX
 PN WO20026617-A1.
 XX
 PD 29-AUG-2002.
 XX
 PF 13-FEB-2002; 2002WO-FI00113.
 XX
 PR 20-FEB-2001; 2001FI-0000323.
 XX
 PA (JURI-) JURILAB LTD OY.
 XX
 PI Salonen J;
 XX
 XX WPI; 2002-667063/71.
 DR P-PSDB; AAE26634.
 XX
 XX Detecting a risk of hypertension and targeting treatment in a subject
 PT by determining the pattern of alleles encoding a variant
 PT alpha-2-adrenoceptor
 XX
 PS Disclosure; Page 27-29; 35pp; English.
 XX
 CC The invention relates to a method for detecting a risk of hypertension
 CC by determining the pattern of alleles encoding a variant alpha-2b-
 CC adrenoceptor (AR) protein. The methods and compositions of the invention
 CC are useful for detecting risks and targeting treatment for hypertension.
 CC The kit is also useful for selecting for clinical drug trials testing
 CC the antihypertensive effect of compounds. The present sequence is human
 CC alpha-2b-adrenoceptor gene.
 XX
 CC Sequence 1353 BP; 223 A; 459 C; 405 G; 266 T; 0 other;
 XX
 SQ
 XX
 XX Query Match 100.0%; Score 20; DB 24; Length 1353;
 XX Best Local Similarity 100.0%; Pred. No. 5.7; 0; Indels 0; Gaps 0;
 XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 AAAAAGCCCAATGACCACAG 20
 DB 1140 AAAAAGCCCAATGACCACAG 1121
 XX
 XX RESULT 8
 XX AAQ14151/C
 XX ID AAQ14151 standard; DNA; 2064 BP.
 XX
 XX AAQ14151;
 AC
 XX 06-JAN-1992 (first entry)
 DT
 XX Human alpha 2 beta adrenergic receptor gene.
 DE
 XX Neurotransmission; adrenaline; epinephrine; NGC-alpha2beta; ss.
 KW
 XX Homo sapiens.
 OS
 XX Key Location/Qualifiers
 FH 288..1752
 FT CDS /*tag= a
 FT
 XX US5053337-A.
 PN
 XX 01-OCT-1991.

XX
 XX 30-OCT-1989; 89US-0428856.
 PF
 XX 30-OCT-1989; 89US-0428856.
 PR
 XX (NEUR-) NEUROGENETIC CORP.
 PA
 XX Weinshank RL, Hartig PR;
 PI
 XX WPI; 1991-110087/42.
 DR P-PSDB; AAR14149.
 XX
 XX Isolated DNA encoding human adrenergic receptor - for detecting
 PT nucleic acids encoding alpha, 2-beta adrenergic receptor, for
 PT screening drugs.
 XX
 PS Claim 1; Fig 2; 15pp; English.
 XX
 CC Clone NGC-alpha2beta was isolated from a human spleen genomic
 CC library by screening with a fragment of the human 5-HT1A receptor
 CC gene. The gene can be used to express recombinant receptor protein
 CC which can be used to produce antibodies for inhibition of receptor
 CC function.
 XX
 SQ Sequence 2064 BP; 319 A; 696 C; 659 G; 390 T; 0 other;
 XX
 XX Query Match 100.0%; Score 20; DB 12; Length 2064;
 XX Best Local Similarity 100.0%; Pred. No. 6; 0; Indels 0; Gaps 0;
 XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 AAAAAGCCCAATGACCACAG 20
 DB 1538 AAAAAGCCCAATGACCACAG 1519
 XX
 XX RESULT 9
 XX AAT59499/C
 XX ID AAT59499 standard; DNA; 2064 BP.
 XX
 XX AAT59499;
 AC
 XX 25-MAR-2003 (updated)
 DT 06-MAY-1997 (first entry)
 DT
 XX Human alpha-2b adrenergic receptor genomic DNA clone.
 DE
 XX Alpha-2b adrenergic receptor; adrenoceptor; adrenaline;
 KW epinephrine; signal transduction; neurotransmitter; ligand; ss.
 KW
 XX Homo sapiens.
 OS
 XX Key Location/Qualifiers
 FH 288..1751
 FT CDS /*tag= a
 FT
 XX US5595880-A.
 PN
 XX 21-JAN-1997.
 PD
 XX 22-OCT-1992; 92US-0965040.
 PF
 XX 30-OCT-1989; 89US-0428856.
 PR 30-MAY-1991; 91US-0707604.
 PR 22-OCT-1992; 92US-0965040.
 XX
 XX (SYNA-) SYNAPTIC PHARM CORP.
 PA
 XX Hartig PR, Weinshank RL;
 PI
 XX WPI; 1997-107576/10.
 DR P-PSDB; AAW11804.
 DR
 XX Assay for alpha-2b adrenergic receptor ligands - using membranes of

FC cells expressing recombinant receptor
 XX Disclosure; Fig 2A-E; 16pp; English.
 XX
 CC A genomic DNA clone (AA15949) codes for human alpha-2B adrenergic
 CC receptor (AA11804), a member of the rhodopsin-like signal transducer
 CC family. It was isolated from a human spleen genomic library in the
 CC lambda vector Charon 28 by screening with a 1.6 kb fragment of the
 CC human 5-hydroxytryptamine receptor gene. Plasmid pNC-alpha-2B
 CC comprising DNA encoding the alpha-2B adrenoceptor is deposited as
 CC ATCC 68144. Vectors have been adapted to allow prodn. of alpha-2B
 CC adrenoceptor in bacterial, yeast or mammalian cells; transfected
 CC Ltk- cells, designated L-NCC-alpha-2B, are deposited as ATCC CTL
 CC 10275. Membranes of such cells can used in novel methods to
 CC identify drugs which specifically interact with, and bind to, the
 CC alpha-2B adrenergic receptor.
 CC (Updated on 25-MAR-2003 to correct PF field.)
 CC
 SQ Sequence 2064 BP; 319 A; 696 C; 659 G; 390 T; 0 other;
 Query Match 100.0%; Score 20; DB 18; Length 2064;
 Best Local Similarity 100.0%; Pred. No. 6;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 AAAAAGCCCAATGACCAAG 20
 DB 1538 AAAAAGCCCAATGACCAAG 1519
 RESULT 10
 ID ACAS6583/C
 AC ACAS6583 standard; CDNA; 2072 BP.
 AC ACAS6583;
 XX
 DT 06-JUN-2003 (first entry)
 XX
 DE Human signalling pathway polynucleotide probe SEQ ID NO 1181.
 XX
 KW Human; probe; ss; array element; Parkinson's disease;
 KW signalling pathway population; cancer; adenocarcinoma; leukaemia;
 KW immunopathy; AIDS; asthma; neuropathy; Alzheimer's disease; microarray.
 XX
 OS Homo sapiens.
 XX
 PN US6500938-B1.
 PD 31-DEC-2002.
 XX
 PF 30-JAN-1998; 98US-0016434.
 XX
 PR 30-JAN-1998; 98US-0016434.
 XX
 PA (INCY-) INCYTE GENOMICS INC.
 XX
 PI Au-Young J, Sellhammer JT;
 XX
 DR WPI; 2003-352189/33.
 XX
 PT Combination of polynucleotide probes, useful as array elements in a
 PT microarray for monitoring the expression of a number of target
 PT polynucleotides -
 XX
 PS Claim 1; SEQ ID NO 1181; 65pp; English.
 XX
 CC The invention relates to a combination which comprises a number of
 CC polynucleotide probes comprising a sequence selected from one of the 1490
 CC sequences mentioned in the specification. The combination is useful as an
 CC array element in a microarray for monitoring the expression of a number
 CC of target polynucleotides. The microarray is particularly useful in the
 CC diagnosis and treatment of cancer and immunopathology and neuropathology.
 CC The microarray is useful in diagnostics and treatment regimens, drug
 CC discovery and development, toxicological and carcinogenicity studies.

CC forensics and pharmacogenomics. The microarray is also useful for
 CC monitoring progression of diseases and for developing sophisticated
 CC profiles for the effects of currently available therapeutic drugs. The
 CC combination is also useful for purifying a subpopulation of mRNA, cDNAs
 CC and genomic fragments and in research and diagnostic applications. The
 CC array can detect changes in expression in a large number of genes coding
 CC for different signalling pathway populations which can be used to diagnose
 CC various diseases including cancer e.g. adenocarcinoma and leukaemia,
 CC immunopathies e.g. AIDS and asthma, neuropathies e.g. Alzheimer's disease
 CC and Parkinson's disease. The present sequence represents a polynucleotide
 CC probe of the invention.
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification but was obtained in electronic format directly from USPTO
 CC at seqdata.uspto.gov/sequence.html?DocID=06500938B1.
 CC
 SQ Sequence 2072 BP; 316 A; 705 C; 660 G; 391 T; 0 other;
 Query Match 100.0%; Score 20; DB 25; Length 2072;
 Best Local Similarity 100.0%; Pred. No. 6;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 AAAAAGCCCAATGACCAAG 20
 DB 1552 AAAAAGCCCAATGACCAAG 1533
 RESULT 11
 ID AB242624/C
 AC AB242624 standard; DNA; 3274 BP.
 AC AB242624;
 XX
 DT 04-MAR-2003 (first entry)
 XX
 DE Human alpha 2b-adrenoceptor nucleotide SEQ ID NO:41.
 XX
 KW G protein-coupled receptor; GPCR; antigenic peptide; gene therapy;
 KW G protein-coupled receptor modulator; antibody; immune-related disease;
 KW growth-related disease; cell regeneration-related disease; AIDS; cancer;
 KW immunological-related cell proliferative disease; autoimmune disease;
 KW Alzheimer's disease; atherosclerosis; infection; osteoarthritis; allergy;
 KW osteoporosis; cardiomyopathy; inflammation; Crohn's disease; diabetes;
 KW graft versus host disease; Parkinson's disease; multiple sclerosis; pain;
 KW psoriasis; anxiety; depression; schizophrenia; dementia; memory loss;
 KW mental retardation; epilepsy; asthma; tuberculosis; obesity; nausea;
 KW hypertension; hypotension; renal disorder; rheumatoid arthritis; trauma;
 KW ulcer; gene; ds.
 XX
 OS Homo sapiens.
 XX
 PN WO200261087-A2.
 PD 08-AUG-2002.
 XX
 PF 19-DEC-2001; 2001WO-US50107.
 XX
 PR 19-DEC-2000; 2000US-257144P.
 XX
 PA (LIFE-) LIFESPAN BIOSCIENCES INC.
 XX
 DR Burner GC, Roush CL, Brown JP;
 XX
 DR WPI; 2003-046718/04.
 DR P-PSDB; ABP81780.
 XX
 PT New isolated antigenic peptides e.g., for G protein-coupled receptors.
 PT (GPCR), useful for diagnosing and designing drugs for treating
 PT conditions in which GPCRs are involved, e.g. AIDS, Alzheimer's disease,
 PT cancer or autoimmune diseases -
 XX
 PS Disclosure; Fig 1; 523pp; English.
 CC
 CC The present invention describes antigenic peptides (1) comprising:

(a) any one of 1601 sequences (see ABP82019 to ABP83619) of 12-24 amino acids. Also described: (1) an assay for the detection of a particular GPCR-coupled receptor (GPCR) or a candidate polypeptide in a sample; and (2) an isolated antibody having high specificity and high affinity or avidity for a particular GPCR. (I) can be used as GPCR modulators and in gene therapy. The antigenic peptides for GPCRs are useful in detecting an antibody against a particular GPCR, and in the production of specific antibodies. The peptides and antibodies are also useful for detecting the presence or absence of corresponding GPCRs. The antigenic peptides for GPCRs and antibodies are useful for diagnosing and designing drugs for treating immune-related diseases, growth-related diseases, cell regeneration-related diseases, immunological-related cell proliferative diseases, or autoimmune diseases, e.g. AIDS, Alzheimer's disease, atherosclerosis, bacterial, fungal, protozoan or viral infections, osteoarthritis, osteoporosis, cancer, cardiomyopathy, chronic and acute inflammation, allergies, Crohn's disease, diabetes, graft versus host disease, Parkinson's disease, multiple sclerosis, pain, psoriasis, anxiety, depression, schizophrenia, dementia, mental retardation, memory loss, epilepsy, asthma, tuberculosis, obesity, nausea, hypertension, hypotension, renal disorders, rheumatoid arthritis, trauma, ulcers, or any other disorder in which GPCRs are involved. The antibodies may be used in immunoassays and immunodiagnosis. AB242523 to AB242869 encode GPCR proteins given in ABP81675 to ABP82018, which are used in the exemplification of the present invention.

Sequence 3274 BP; 587 A; 979 C; 967 G; 741 T; 0 other;

Query Match 100.0%; Score 20; DB 25; Length 3274;
Best Local Similarity 100.0%; Pred. No. 6.3;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 AAAAGGCCCATGACCAAG 20
1140 AAAAGGCCCATGACCAAG 1121

RESULT 12
ABN98529/C
ID ABN98529 standard; DNA; 965 BP.
XX
AC ABN98529;
XX
DT 01-AUG-2002 (first entry)
XX
DE Arabidopsis thaliana expressed polynucleotide SEQ ID NO 297.
XX
KM Arabidopsis thaliana; plant; insecticide; fungicide; transgenic; stress;
KM disease; crop; thale cress; tolerance factor; insect; pathogen;
KM nutrition; ds.
XX
OS Arabidopsis thaliana.
XX
PN US2002023281-A1.
XX
PD 21-FEB-2002.
XX
PF 26-JAN-2001; 2001US-0770445.
XX
PR 27-JAN-2000; 2000US-178472P.
XX
PA (GORL/) GORLACH J.
PA (ANY/) AN Y.
PA (HAMI/) HAMILTON C M.
PA (PRIC/) PRICE J L.
PA (RAIN/) RAINES T M.
PA (YUY/) YU Y.
PA (RAME/) RAMEAKA J G.
PA (PAGE/) PAGE A.
PA (MATH/) MATHEN A V.
PA (LEDF/) LEDFORD B L.
PA (WOES/) WOESSNER J P.
PA (HAAS/) HAAS W D.
PA (GARC/) GARCIA C A.

(KRIC/) KRICKER M.
PA (SLAT/) SLATER T.
PA (DAVI/) DAVIS K R.
PA (ALLE/) ALLEN K.
PA (HOFF/) HOFFMAN N.
PA (HURB/) HURBAN P.
XX
PI Gorlach J, An Y, Hamilton CM, Price JL, Raines TM, Yu Y;
PI Rameaka JG, Page A, Mathew AV, Ledford BL, Woessner JP, Haas WD;
PI Garcia CA, Kricker M, Slater T, Davis KR, Allen K, Hoffman N;
PI Hurban P;
XX
XX WPI; 2002-400781/43.
XX
DR New Arabidopsis thaliana nucleic acid for identifying homologous genes,
XX producing compositions that modulate the expression or function of its
XX encoded protein, and mapping functional regions of protein
XX
XX Claim 1; SEQ ID NO 297; 49pp + Sequence Listing; English.
XX
PS The invention relates to an Arabidopsis thaliana nucleic acid (I)
XX comprising a sequence capable of hybridizing under stringent conditions
XX to a sequence selected from any one of 999 sequences (ABN98233-ABN99231),
XX given in the specification or its fragment. A polypeptide (II) encoded by
XX (I), a transgenic plant (III) comprising an exogenous nucleic acid or a
XX genetically modified cell (IV) comprising an exogenous nucleic acid, is
XX useful for screening a candidate agent for its biological effect. (I) is
XX useful in identifying homologous or related genes, in producing
XX compositions that modulate the expression or function of its encoded
XX protein, mapping functional regions of the protein and in studying
XX associated physiological pathways. (I) is also useful for the genetic
XX manipulation of cells, particularly plant cells. (I) is also useful in
XX screening assays of various plant strains to determine the strains that
XX are best capable of withstanding a particular disease or environmental
XX stress. (II) and (III) are useful for screening of biologically active
XX agents, e.g. fungicides, insecticides, etc., for elucidating biochemical
XX pathways. The screened agents are useful in improved methods of treating
XX crops to prevent or treat disease. (II) are also useful in screening
XX programs to identify agents that mimic or enhance the action of tolerance
XX factors. Such agents are useful in improved methods of treating crops to
XX enhance their tolerance to environmental stress. (I) is also useful
XX for enhancing or inhibiting production of a biosynthetic product in a
XX plant. (III) is useful for identifying other mediators that may induce
XX expression of proteins of interest, for establishing the extent to which
XX any specific insect and/or pathogen is responsible for damage to a
XX particular plant, for identifying other mediators that enhance or induce
XX tolerance to environmental stress, for identifying factors involved in
XX biosynthetic pathways of nutritional, commercial, or medicinal value and
XX for identifying productions of nutritional, commercial or medicinal
XX value. (IV) is useful in the study of genetic function and regulation,
XX for alteration of the cellular metabolism and for screening compounds
XX that may affect the biological function of the gene or gene products.
XX Note: The sequence data for this patent did not form part of the printed
XX specification, but was obtained in electronic format directly from USPTO
XX at seqdata.uspto.gov/sequence.html?DocID=999909770445.

Sequence 965 BP; 218 A; 314 C; 161 G; 268 T; 4 other;

Query Match 87.0%; Score 17.4; DB 24; Length 965;
Best Local Similarity 94.7%; Pred. No. 95;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

2 AAAAGGCCCATGACCAAG 20
219 AAAAGGCCCATGACCAAG 201

RESULT 13
ABL03674
ID ABL03674 standard; cDNA; 4910 BP.
XX
AC ABL03674;
XX

DT 26-MAR-2002 (first entry)
 XX Drosophila melanogaster expressed polynucleotide seq ID NO 5504.
 DE
 XX
 XX Drosophila; developmental biology; cell signalling; insecticide;
 KM pharmaceutical; gene; ss.
 XX
 OS Drosophila melanogaster.
 XX
 PN W0200171042-A2.
 XX
 PD 27-SEP-2001.
 XX
 PF 23-MAR-2001; 2001WO-US09231.
 XX
 PR 23-MAR-2000; 2000US-191637P.
 XX
 PR 11-JUL-2000; 2000US-0614150.
 XX
 PA (PEKE) PE CORP NY.
 XX
 PI Venter JC, Adams M, Li FWD, Myers EW,
 XX
 PI WPI; 2001-656860/75.
 XX
 DR P-PSDB; ABB5957L.
 XX
 XX New isolated nucleic acid detection reagent for detecting 1000 or more
 PT genes from Drosophila and for elucidating cell signalling and cell-cell
 PT interactions -
 XX
 PS Claim 1, SEQ ID NO 5504; 21pp + Sequence Listing; English.
 XX
 XX The invention relates to an isolated nucleic acid detection reagent
 CC capable of detecting 1000 or more genes from Drosophila. The invention is
 CC useful in developmental biology and in elucidating cell signalling and
 CC cell-cell interactions in higher eukaryotes for the development of
 CC insecticides, therapeutics and pharmaceutical drugs. The invention
 CC discloses genomic DNA sequences (AB116176-AB130511), expressed DNA
 CC sequences (AB101840-AB116175) and the encoded proteins
 CC (ABB57737-ABB72072).
 CC The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.
 CC
 XX Sequence 4910 BP; 1279 A; 1083 C; 1134 G; 1414 T; 0 other;
 SQ
 Query Match 87.0%; Score 17.4; DB 23; Length 4910;
 Best Local Similarity 94.7%; Pred. No. 1.1e+02;
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 AAAAAGCCCATGACACACA 19
 Db 2828 AAAAAGCCCATGACACACA 2846
 RESULT 14
 AAT48444/c
 ID AAT48444 standard; cDNA; 1441 BP.
 XX
 AC AAT48444;
 XX
 DT 11-APR-1997 (first entry)
 XX
 DE Human TGF-beta-like cytokine pCL13 variant u2.
 XX
 KM pCL13; clone 13; transforming growth factor-beta; TGF-beta;
 KM immunosuppressive; cell differentiation; antiproliferative;
 KM wound healing; vulnery; ischaemic injury; inflammation; cancer;
 KM autoimmune disease; fibrotic disease; diagnosis; gene therapy; ss.
 XX
 OS Homo sapiens.
 XX
 XX Key Location/Qualifiers
 FH CDS 234..1160

FT /*tag= a
 XX
 PN W09700958-A1.
 XX
 PD 09-JAN-1997.
 XX
 PF 24-JUN-1996; 96WO-AU00386.
 XX
 PR 09-FEB-1996; 96AU-0007983.
 XX
 PR 22-JUN-1995; 95AU-0003706.
 XX
 PR 23-AUG-1995; 95AU-0004990.
 XX
 PA (SVIN-) ST VINCENT'S HOSPITAL SYDNEY LTD.
 XX
 PI Bootcov M, Breit S;
 XX
 DR WPI; 1997-087385/08.
 XX
 DR P-PSDB; AAM10668.
 XX
 XX Isolated nucleic acid encoding pCL13, new TGF-beta family member -
 PT has immunosuppressant, cell differentiation promoting and
 PT antiproliferative activities, for treatment of wounds, ischaemic
 PT injury, cancer, inflammatory disease etc.
 XX
 PS Example 17, Fig 20A, 73pp; English.
 XX
 XX cDNA clones b2, b1, u2, f1, a1, b1, d2 and d02 (AAT48442-49) are
 CC variants of clone 13 (AAT48438), which codes for pCL13 (AAM10662), a
 CC novel TGF-beta-like cytokine whose activities include
 CC immunosuppression, down-regulation of leucocyte extravasation and
 CC motility, promotion of cell differentiation and inhibition of
 CC proliferation. The clones were obtd. from a foetal lung library
 CC using a portion of the coding region of clone 13 (see also AAT48438)
 CC as probe. They show substantial variation in the 5' untranslated
 CC region but only minor differences in the coding region. Translated
 CC coding regions are given in AAM10666-73. While the variants may be
 CC important in e.g. transcriptional regulation they are untranslated
 CC and hence cannot affect bioactivity.
 XX
 SQ Sequence 1441 BP; 300 A; 451 C; 428 G; 262 T; 0 other;
 Query Match 84.0%; Score 16.8; DB 18; Length 1441;
 Best Local Similarity 90.0%; Pred. No. 1.9e+02;
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 AAAAAGCCCATGACACAG 20
 Db 110 AAAAAGCCCATGACACAG 91
 RESULT 15
 AAT48442/c
 ID AAT48442 standard; cDNA; 2177 BP.
 XX
 AC AAT48442;
 XX
 DT 11-APR-1997 (first entry)
 XX
 DE Human TGF-beta-like cytokine pCL13 variant b2.
 XX
 KM pCL13; clone 13; transforming growth factor-beta; TGF-beta;
 KM immunosuppressive; cell differentiation; antiproliferative;
 KM wound healing; vulnery; ischaemic injury; inflammation; cancer;
 KM autoimmune disease; fibrotic disease; diagnosis; gene therapy; ss.
 XX
 OS Homo sapiens.
 XX
 XX Key Location/Qualifiers
 FH CDS 993..1919
 FT /*tag= a
 XX
 XX W09700958-A1.
 XX

```

PD 09-JAN-1997.
XX
XX 24-JUN-1996; 96WO-AU00386.
XX
XX 09-FEB-1996; 96AU-0007983.
PR 22-JUN-1995; 95AU-0003706.
PR 23-AUG-1995; 95AU-0004990.
XX
XX (SVIN-) ST VINCENT'S HOSPITAL SYDNEY LTD.
XX
XX
XX Bootcov M, Breit S;
XX
XX WPI; 1997-087385/08.
DR P-PSDB; AAW10666.
XX
XX Isolated nucleic acid encoding pCL13, new TGF-beta family member -
PT has immunosuppressant, cell differentiation promoting and
PT anti-proliferative activities, for treatment of wounds, ischaemic
PT injury, cancer, inflammatory disease etc.
XX
XX
XX Example 17; Fig 20A; 73pp; English.
XX
XX cDNA clones b2, h1, u2, f1, a1, b1, d2 and dd2 (AA148442-49) are
XX variants of clone 13 (AA148438), which codes for pCL13 (AAW10662), a
XX novel TGF-beta-like cytokine whose activities include
XX immunosuppression, down-regulation of leucocyte extravasation and
XX motility, promotion of cell differentiation and inhibition of
XX proliferation. The clones were obtd. from a foetal lung library
XX using a portion of the coding region of clone 13 (see also AA148438)
XX as probe. They show substantial variation in the 5' untranslated
XX region but only minor differences in the coding region. Translated
XX coding regions are given in AAW10666-73. While the variants may be
XX important in e.g. transcriptional regulation they are untranslated
XX and hence cannot affect bioactivity.
XX
XX Sequence 2177 BP; 462 A; 645 C; 609 G; 461 T; 0 other;
SQ
Query Match 84.0%; Score 16.8; DB 18; Length 2177;
Best Local Similarity 90.0%; Pred. No. 2e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 AAAAAGCCCAATGACCACAG 20
DB 869 AAACACTCCCAATGACCACAG 850

```

Search completed: February 12, 2004, 04:01:34
 Job time : 108.122 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using bw model

Run on: February 12, 2004, 04:01:41 ; Search time 27.3171 Seconds
(without alignments)
323.156 Million cell updates/sec

Title: US-09-692-077D-16
Perfect score: 20
Sequence: 1 aaacagccatgaccacag 20

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents NA:
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2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/2/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/2/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/2/ina/PTCUS_COMB.seq:*
6: /cgn2_6/ptodata/2/ina/backfile1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	20	100.0	2072 4	US-09-016-434-1181 Sequence 1181, Ap
2	16	80.0	36941 4	US-08-111-731A-130 Sequence 130, App
3	15.2	76.0	1593 4	US-09-134-001C-1673 Sequence 1673, Ap
4	15.2	76.0	1779 4	US-09-328-352-312 Sequence 312, App
5	15.2	76.0	5820 3	US-09-029-213B-7 Sequence 7, Appli
6	15.2	76.0	6755 3	US-08-931-999-4 Sequence 4, Appli
7	15.2	76.0	55827 4	US-09-813-133A-3 Sequence 3, Appli
8	14.8	74.0	215 4	US-09-177-650-103 Sequence 103, App
9	14.8	74.0	268 3	US-09-321-298-106 Sequence 106, App
10	14.8	74.0	291 4	US-09-313-294A-6186 Sequence 6186, Ap
11	14.8	74.0	24 4	US-08-169-715-1 Sequence 1, Appli
12	14.8	74.0	1422 4	US-09-328-352-3388 Sequence 3388, Ap
13	14.8	74.0	124884 4	US-09-661-596A-76 Sequence 76, Appli
14	14.4	72.0	1788 4	US-09-328-352-1004 Sequence 1004, Ap
15	14.4	72.0	1858 2	US-08-359-705B-7 Sequence 7, Appli
16	14.4	72.0	1858 2	US-08-286-846A-7 Sequence 7, Appli
17	14.4	72.0	1858 2	US-08-457-880A-7 Sequence 7, Appli
18	14.4	72.0	1858 3	US-08-444-622A-7 Sequence 7, Appli
19	14.4	72.0	1858 3	US-08-942-562-7 Sequence 7, Appli
20	14.4	72.0	1858 3	US-09-156-923-7 Sequence 7, Appli
21	14.4	72.0	2715 2	US-08-359-705B-5 Sequence 5, Appli
22	14.4	72.0	2715 2	US-08-286-846A-5 Sequence 5, Appli
23	14.4	72.0	2715 2	US-08-457-880A-5 Sequence 5, Appli
24	14.4	72.0	2715 3	US-08-444-622A-5 Sequence 5, Appli
25	14.4	72.0	2715 3	US-08-942-562-5 Sequence 5, Appli
26	14.4	72.0	2715 3	US-09-156-923-5 Sequence 5, Appli
27	14.4	72.0	2940 1	US-08-286-305A-8 Sequence 8, Appli

C 28	14.4	72.0	2940 2	US-08-441-104A-8	Sequence 8, Appli
C 29	14.4	72.0	2940 2	US-08-440-816A-8	Sequence 8, Appli
C 30	14.4	72.0	2940 3	US-09-417-381A-8	Sequence 8, Appli
C 31	14.2	71.0	186 4	US-09-313-294A-1872	Sequence 1872, Ap
C 32	14.2	71.0	273 4	US-09-134-001C-2061	Sequence 2061, Ap
C 33	14.2	71.0	273 4	US-09-107-532A-583	Sequence 583, Ap
C 34	14.2	71.0	278 4	US-09-313-294A-885	Sequence 885, App
C 35	14.2	71.0	294 4	US-09-134-001C-2032	Sequence 2032, Ap
C 36	14.2	71.0	390 4	US-09-134-001C-2684	Sequence 2684, Ap
C 37	14.2	71.0	426 1	US-07-661-610C-12	Sequence 12, Appli
C 38	14.2	71.0	534 4	US-09-328-352-937	Sequence 937, App
C 39	14.2	71.0	609 4	US-09-134-001C-2780	Sequence 2780, Ap
C 40	14.2	71.0	840 4	US-09-328-352-1188	Sequence 1188, Ap
C 41	14.2	71.0	865 1	US-08-341-568-4	Sequence 4, Appli
C 42	14.2	71.0	865 2	US-08-911-020-4	Sequence 4, Appli
C 43	14.2	71.0	1008 4	US-09-107-532A-3178	Sequence 3178, Ap
C 44	14.2	71.0	1031 4	US-09-397-787-157	Sequence 157, App
C 45	14.2	71.0	1341 2	US-08-945-848-7	Sequence 7, Appli

ALIGNMENTS

RESULT 1
US-09-016-434-1181/C
; Sequence 1181, Application US/09016434
; Patent No. 6500938
; GENERAL INFORMATION:
; APPLICANT: Janice Au-Young
; APPLICANT: Jeffrey J. Seilhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
; TITLE OF INVENTION: PATHWAY GENE EXPRESSION
; NUMBER OF SEQUENCES: 1490
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/016,434
; FILING DATE: HEREWITH
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, Karen J.
; REGISTRATION NUMBER: 37,071
; REFERENCE/DOCKET NUMBER: PA-0002 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 1181:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2072 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GENBANK
; CLONE: 9178197
; US-09-016-434-1181
Query Match 100.0%; Score 20; DB 4; Length 2072;
Best Local Similarity 100.0%; Pred. No. 0.63;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AAAAAGCCCATGACCCACAG 20
|||||
Db 1552 AAAAAGCCCATGACCCACAG 1533

RESULT 2
US-08-311-731A-130
; Sequence 130, Application US/08311731A
; Patent No. 6583266
; GENERAL INFORMATION:
; APPLICANT: SMITH, DOUGLAS
; APPLICANT: MAO, JEN-I
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES
; TITLE OF INVENTION: RELATING TO MYCOBACTERIUM TUBERCULOSIS AND LAPRAE FOR
; TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
; NUMBER OF SEQUENCES: 411
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: WOLF, GREENFIELD & SACKS, P.C.
; STREET: 600 ATLANTIC AVENUE
; CITY: BOSTON
; STATE: MASSACHUSETTS
; COUNTRY: USA
; ZIP: 02210

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/08/311,731A
APPLICATION DATA:
FILING DATE:
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: GATES, EDWARD R.
REGISTRATION NUMBER: 31,616
REFERENCE/DOCKET NUMBER: C0044/7125
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/720-3500
TELEFAX: 617/720-2441
INFORMATION FOR SEQ ID NO: 130:
SEQUENCE CHARACTERISTICS:
LENGTH: 36941 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: MYCOBACTERIUM LEPRAE
US-08-311-731A-130

Query Match 80.0%; Score 16; DB 4; Length 36941;
Best Local Similarity 100.0%; Pred. No. 97;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 5 ACGCCATGACCCACAG 20
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Db 26433 ACGCCATGACCCACAG 26448

RESULT 3
US-09-134-001C-1673/C
; Sequence 1673, Application US/09134001C
; Patent No. 6389370
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
; TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: GTC-007
; CURRENT APPLICATION NUMBER: US/09/134,001C

; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/064,964
; PRIOR FILING DATE: 1997-11-08
; PRIOR APPLICATION NUMBER: US 60/055,779
; PRIOR FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 5674
; SEQ ID NO 1673
; LENGTH: 1593
; TYPE: DNA
; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-1673

Query Match 76.0%; Score 15.2; DB 4; Length 1593;
Best Local Similarity 85.0%; Pred. No. 1.4e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 AAAAAGCCCATGACCCACAG 20
|||||
Db 1170 AAAAAGCCCATGACCCACAG 1151

RESULT 4
US-09-328-352-312
; Sequence 312, Application US/09328352
; Patent No. 6562958
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
; FILE REFERENCE: GTC99-03PA
; CURRENT APPLICATION NUMBER: US/09/328,352
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 312
; LENGTH: 1779
; TYPE: DNA
; ORGANISM: Acinetobacter baumannii
US-09-328-352-312

Query Match 76.0%; Score 15.2; DB 4; Length 1779;
Best Local Similarity 85.0%; Pred. No. 1.4e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 AAAAAGCCCATGACCCACAG 20
|||||
Db 1377 AAAAAGCCCATGACCCACAG 1396

RESULT 5
US-09-029-213B-7/C
; Sequence 7, Application US/09029213B
; Patent No. 6180098
; GENERAL INFORMATION:
; APPLICANT: CHRISTIAN, Peter D.
; TITLE OF INVENTION: RECOMBINANT HELICOVERPA BACULOVIRUSES
; TITLE OF INVENTION: EXPRESSING HETEROLOGOUS DNA
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McDermott, Will & Emery
; STREET: 600 13th Street, NW
; CITY: Washington
; STATE: District of Columbia
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/029,213B
; FILING DATE: 31-AUG-1998
; CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:
NAME: Joseph Hyosuk Kim
REGISTRATION NUMBER: 41,425
REFERENCE/DOCKET NUMBER: 50179-048
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-756-8000
TELEFAX: 202-756-8087
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 5820 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 1388..1973
FEATURE:
NAME/KEY: CDS
LOCATION: 2083..2820
FEATURE:
NAME/KEY: CDS
LOCATION: 4074..4875
FEATURE:
NAME/KEY: CDS
LOCATION: complement (5..317)
FEATURE:
NAME/KEY: CDS
LOCATION: complement (651..1194)
FEATURE:
NAME/KEY: CDS
LOCATION: complement (2821..3790)
FEATURE:
NAME/KEY: CDS
LOCATION: complement (5004..5820)
US-09-029-213B-7

Query Match
Best Local Similarity 76.0%; Score 15.2; DB 3; Length 5820;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 AAAAAGCCCAATGACCACAG 20
Db 110 AATAAGCCATGATGACACG 91

RESULT 6
US-08-931-999-4
Sequence 4, Application US/08931999
Patent No. 6043219
GENERAL INFORMATION:
APPLICANT: Iandolo, John J.
APPLICANT: Crupper, Scott S.
TITLE OF INVENTION: Broad Spectrum Chemotherapeutic Peptide
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hovey, Williams, Timmons & Collins
STREET: 2405 Grand Boulevard, Suite 400
CITY: Kansas City
STATE: Missouri
COUNTRY: U.S.A.
ZIP: 64108
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/931,999
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/710,561

FILING DATE: 19-SEP-1996
ATTORNEY/AGENT INFORMATION:
NAME: Collins, John M.
REGISTRATION NUMBER: 26,262
REFERENCE/DOCKET NUMBER: 25043-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 816/474-9050
TELEFAX: 816/474-9057
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 6755 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Staphylococcus aureus
STRAIN: UT0007
US-08-931-999-4

Query Match
Best Local Similarity 76.0%; Score 15.2; DB 3; Length 6755;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 AAAAAGCCCAATGACCACAG 20
Db 2263 AAAAAGCAAGACACACAG 2282

RESULT 7
US-09-813-133A-3
Sequence 3, Application US/09813133A
Patent No. 6455294
GENERAL INFORMATION:
APPLICANT: GAN, weiniu et al
TITLE OF INVENTION: ISOLATED HUMAN PROTEASE PROTEINS,
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PROTEASE PROTEINS, AND
TITLE OF INVENTION: USES THEREOF
FILE REFERENCE: CL001173
CURRENT APPLICATION NUMBER: US/09/813,133A
CURRENT FILING DATE: 2001-06-06
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 3 55827
LENGTH: 55827
TYPE: DNA
ORGANISM: Human
US-09-813-133A-3

Query Match
Best Local Similarity 76.0%; Score 15.2; DB 4; Length 55827;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 AAAAAGCCCAATGACCACAG 20
Db 21190 AAAAGGCACTGACCACAG 21209

RESULT 8
US-09-177-650-103/C
Sequence 103, Application US/09177650
Patent No. 6413719
GENERAL INFORMATION:
APPLICANT: Leppert, Mark F.
APPLICANT: Singh, Nanda
APPLICANT: Charlier, Carole
TITLE OF INVENTION: KCNO2 AND KCNO3 - POTASSIUM CHANNEL GENES WHICH ARE
TITLE OF INVENTION: MUTATED IN BENIGN FAMILIAL NEONATAL CONVULSIONS (BFNC)
TITLE OF INVENTION: AND OTHER EPILEPSIES
FILE REFERENCE: 2323-134
CURRENT APPLICATION NUMBER: US/09/177,650

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/ CURRENT FILING DATE: 1998-10-23
/ EARLIER APPLICATION NUMBER: 60/063,147
/ EARLIER FILING DATE: 1997-10-24
/ NUMBER OF SEQ ID NOS: 129
/ SOFTWARE: Patentn Ver. 2.0
/ SEQ ID NO: 103
/ LENGTH: 215
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-09-177-650-103
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Query Match      74.0%; Score 14.8; DB 4; Length 215;
Best Local Similarity 88.9%; Pred. No. 1.6e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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QY      2 AAAACGCCAATGACCACA 19
Db      146 AAAACCAATGACCACA 129
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```
RESULT 9
US-09-221-298-106
/ Sequence 106, Application US/09221298
/ Patent No. 6284241
/ GENERAL INFORMATION:
/ APPLICANT: Xu, Jiaqichun
/ TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THERAPY AND DIAGNOSIS
/ FILE REFERENCE: 210121.471
/ CURRENT APPLICATION NUMBER: US/09/221,298
/ CURRENT FILING DATE: 1998-12-23
/ NUMBER OF SEQ ID NOS: 112
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO: 106
/ LENGTH: 268
/ TYPE: DNA
/ ORGANISM: Human
/ FEATURE:
/ NAME/KEY: modified_base
/ LOCATION: (118)
/ OTHER INFORMATION: Where n is a, c, g or t
/ FEATURE:
/ NAME/KEY: modified_base
/ LOCATION: (73)
/ OTHER INFORMATION: Where n is a, c, g or t
/ FEATURE:
/ NAME/KEY: modified_base
/ LOCATION: (96)
/ OTHER INFORMATION: Where n is a, c, g or t
/ FEATURE:
/ NAME/KEY: modified_base
/ LOCATION: (113)
/ OTHER INFORMATION: Where n is a, c, g or t
/ FEATURE:
/ NAME/KEY: modified_base
/ LOCATION: (161)
/ OTHER INFORMATION: Where n is a, c, g or t
/ FEATURE:
/ NAME/KEY: modified_base
/ LOCATION: (195)
/ OTHER INFORMATION: Where n is a, c, g or t
/ FEATURE:
/ NAME/KEY: modified_base
/ LOCATION: (219)
/ OTHER INFORMATION: Where n is a, c, g or t
/ FEATURE:
/ NAME/KEY: modified_base
/ LOCATION: (247)
/ OTHER INFORMATION: Where n is a, c, g or t
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/ FEATURE:
/ NAME/KEY: modified_base
/ LOCATION: (250)
/ OTHER INFORMATION: Where n is a, c, g or t
/ FEATURE:
/ NAME/KEY: modified_base
/ LOCATION: (255)
/ OTHER INFORMATION: Where n is a, c, g or t
/ FEATURE:
/ NAME/KEY: modified_base
/ LOCATION: (257)
/ OTHER INFORMATION: Where n is a, c, g or t
US-09-221-298-106
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Query Match      74.0%; Score 14.8; DB 3; Length 268;
Best Local Similarity 88.9%; Pred. No. 1.6e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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QY      1 AAAACGCCAATGACCACC 18
Db      200 AAAACGCCAATGAACCC 217
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RESULT 10
US-09-313-294A-6186
/ Sequence 6186, Application US/09313294A
/ Patent No. 6476212
/ GENERAL INFORMATION:
/ APPLICANT: Lalgudi, Raghunath V.
/ APPLICANT: Ito, Laura Y.
/ APPLICANT: Sherman, Bradley K.
/ TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN EAR
/ FILE REFERENCE: PL-0017 US
/ CURRENT APPLICATION NUMBER: US/09/313,294A
/ CURRENT FILING DATE: 1999-05-14
/ NUMBER OF SEQ ID NOS: 7600
/ SOFTWARE: PERL Program
/ SEQ ID NO: 6186
/ LENGTH: 291
/ TYPE: DNA
/ ORGANISM: Zea mays
/ FEATURE:
/ NAME/KEY: misc feature
/ OTHER INFORMATION: Incycle ID No. 6476212 700351368H1
/ NAME/KEY: unsure
/ LOCATION: 264, 286
/ OTHER INFORMATION: a, t, c, g, or other
US-09-313-294A-6186
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```
Query Match      74.0%; Score 14.8; DB 4; Length 291;
Best Local Similarity 88.9%; Pred. No. 1.6e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
QY      2 AAAACGCCAATGACCACA 19
Db      172 AAAACGCCAATGACCATA 189
```

```
RESULT 11
US-08-169-715-1/c
/ Sequence 1, Application US/08169715
/ Patent No. 6300056
/ GENERAL INFORMATION:
/ APPLICANT: Irvine, Bruce D.
/ APPLICANT: Horn, Thomas
/ APPLICANT: Chang, Chu-An
/ TITLE OF INVENTION: HIV PROBES FOR USE IN SOLUTION PHASE
/ NUMBER OF SEQUENCES: 63
/ CORRESPONDENCE ADDRESSES:
/ ADDRESSEE: Morrison & Foerster
/ STREET: 545 Middlefield Road, Suite 200
/ CITY: Menlo Park
```

STATE: California
COUNTRY: USA
ZIP: 94025
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/169,715
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/813,583
FILING DATE: 18-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: Monroy, Gladys H.
REGISTRATION NUMBER: 32,430
REFERENCE/DOCKET NUMBER: 22300-20150.00
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-813-5600
TELEFAX: 415-327-2951
TELEX: 706141
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 24 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-169-715-1

Query Match 74.0%; Score 14.8; DB 4; Length 24;
Best Local Similarity 66.7%; Pred. No. 1.9e+02;
Matches 8; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 5 ACGCCATGACC 16
DB 24 AGGCATAGGACC 13

RESULT 12
US-09-328-352-3388/c
Sequence 3388, Application US/09328352
Patent No. 6562958
GENERAL INFORMATION:
APPLICANT: Gary L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
FILE REFERENCE: BAUMANNIT FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
SEQ ID NO 3388
LENGTH: 1422
TYPE: DNA
ORGANISM: Acinetobacter baumannii
US-09-328-352-3388

Query Match 74.0%; Score 14.8; DB 4; Length 1422;
Best Local Similarity 88.9%; Pred. No. 2.2e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 AAAGCCATGACACAG 20
DB 1178 AAAGCCACTGACACAG 1161

RESULT 13
US-09-661-596A-76/c
Sequence 76, Application US/09661596A
Patent No. 652806
GENERAL INFORMATION:
APPLICANT: Grose, Charles

APPLICANT: Santos, Richard
TITLE OF INVENTION: VARIANT VARICELLA-ZOSTER VIRUSES AND METHODS OF USE
FILE REFERENCE: 140,0011 0101
CURRENT APPLICATION NUMBER: US/09/661,596A
CURRENT FILING DATE: 2000-09-14
PRIOR APPLICATION NUMBER: US 60/153,779
PRIOR FILING DATE: 1999-09-14
NUMBER OF SEQ ID NOS: 80
SOFTWARE: Patent in version 3.0
SEQ ID NO 76
LENGTH: 124884
TYPE: DNA
ORGANISM: Varicella zoster
US-09-661-596A-76

Query Match 74.0%; Score 14.8; DB 4; Length 124884;
Best Local Similarity 88.9%; Pred. No. 4.3e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 AAAGCCATGACACAG 20
DB 46128 AATGCCATGTCACAG 46111

RESULT 14
US-09-328-352-1004
Sequence 1004, Application US/09328352
Patent No. 6562958
GENERAL INFORMATION:
APPLICANT: Gary L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
FILE REFERENCE: BAUMANNIT FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
SEQ ID NO 1004
LENGTH: 1788
TYPE: DNA
ORGANISM: Acinetobacter baumannii
US-09-328-352-1004

Query Match 72.0%; Score 14.4; DB 4; Length 1788;
Best Local Similarity 93.8%; Pred. No. 3.5e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AAAAAAGCCATGACC 16
DB 1156 AAAAAAGCCATGACC 1171

RESULT 15
US-08-359-705B-7/c
Sequence 7, Application US/08359705B
Patent No. 5844092
GENERAL INFORMATION:
APPLICANT: Presta, Leonard G.
APPLICANT: Shelton, David L.
APPLICANT: Utter, Roman
TITLE OF INVENTION: Human Trk Receptors and Neurotrophic Factor Inhibitors
NUMBER OF SEQUENCES: 41
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)

;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/359,705B
; FILING DATE: 20-Dec-1994
; CLASSIFICATION: 424
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: 08/286846
; FILING DATE: 08/10/94
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: 08/215139
; FILING DATE: 03/18/94
; ATTORNEY/AGENT INFORMATION:
; NAME: Torchia, Ph.D., Timothy E.
; REGISTRATION NUMBER: 36,700
; REFERENCE/DOCKET NUMBER: P0873P2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-8674
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1858 base pairs
; TYPE: Nucleic Acid
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; US-08-359-705B-7

Query Match 72.0%; Score 14.4; DB 2; Length 1858;
Best Local Similarity 93.8%; Pred. No. 3.6e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 5 ACCGCAATGACCAAG 20
| | | | | | | | | | | | | | | | | | | | | |
Db 1529 ATGCAATGACCAAG 1514

Search completed: February 12, 2004, 06:08:16
Job time : 33.3171 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Comphen Ltd.

OM nucleic - nucleic search, using BW model

Run on: February 12, 2004, 04:42:03 ; Search time 113.659 Seconds
(without alignments)
648.193 Million cell updates/sec

Title: US-09-692-077D-16

Perfect score: 20
Sequence: 1 aaacgccaatgaccacag 20

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 2449703 seqs, 1841816367 residues

Total number of hits satisfying chosen parameters: 4899406

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

Published Applications_NA.*
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18: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	20	100.0	20	US-10-001-073-16	Sequence 16, Appl
2	20	100.0	1344	9 US-09-825-923-1	Sequence 1, Appl
3	20	100.0	1344	15 US-10-077-870-1	Sequence 1, Appl
4	20	100.0	1344	15 US-10-001-073-2	Sequence 2, Appl
5	20	100.0	1344	9 US-09-825-923-3	Sequence 3, Appl
6	20	100.0	1353	15 US-10-077-870-3	Sequence 3, Appl
7	20	100.0	1353	15 US-10-001-073-1	Sequence 1, Appl
8	20	100.0	2072	12 US-10-305-720-1181	Sequence 1181, Ap
9	20	100.0	3274	15 US-10-225-567A-41	Sequence 41, Appl
10	17.4	87.0	965	9 US-09-770-445-297	Sequence 297, Appl
11	16.8	84.0	1767	12 US-10-369-493-42551	Sequence 42551, A
12	16.4	82.0	788	12 US-10-398-221-1266	Sequence 1266, Ap
13	16.4	82.0	996	10 US-09-738-626-743	Sequence 743, Appl
14	16.4	82.0	1282	12 US-10-292-798-1745	Sequence 1745, Ap
15	16.4	82.0	1282	13 US-10-017-161-2099	Sequence 2099, Ap

16	16.4	82.0	4504	12 US-10-398-221-3790	Sequence 3790, Ap
17	16.4	82.0	3309400	10 US-09-738-626-1	Sequence 1, Appl
18	16.4	82.0	766	13 US-10-027-632-156514	Sequence 156514, A
19	16.4	82.0	766	14 US-10-027-632-156514	Sequence 156514, A
20	16.4	82.0	802	13 US-10-027-632-156512	Sequence 156512, A
21	16.4	82.0	802	13 US-10-027-632-156513	Sequence 156513, A
22	16.4	82.0	802	14 US-10-027-632-156512	Sequence 156512, A
23	16.4	82.0	802	14 US-10-027-632-156513	Sequence 156513, A
24	15.8	79.0	492	13 US-10-027-632-33956	Sequence 83956, A
25	15.8	79.0	492	13 US-10-027-632-33957	Sequence 83957, A
26	15.8	79.0	492	13 US-10-027-632-298547	Sequence 298547, A
27	15.8	79.0	492	13 US-10-027-632-298548	Sequence 298548, A
28	15.8	79.0	492	14 US-10-027-632-83956	Sequence 83956, A
29	15.8	79.0	492	14 US-10-027-632-83957	Sequence 83957, A
30	15.8	79.0	492	14 US-10-027-632-298547	Sequence 298547, A
31	15.8	79.0	492	14 US-10-027-632-298548	Sequence 298548, A
32	15.8	79.0	840	12 US-10-191-803-211	Sequence 211, Appl
33	15.8	79.0	870	12 US-10-369-493-37126	Sequence 37126, A
34	15.8	79.0	1116	12 US-10-447-328-31	Sequence 31, Appl
35	15.8	79.0	1374	15 US-10-001-073-42	Sequence 42, Appl
36	15.8	79.0	1386	15 US-10-001-073-40	Sequence 40, Appl
37	15.8	79.0	1758	13 US-10-101-510-450	Sequence 450, Appl
38	15.8	79.0	2000	10 US-09-938-842A-4905	Sequence 4905, Appl
39	15.8	79.0	2000	12 US-09-938-842A-4905	Sequence 4905, Appl
40	15.8	79.0	2826	15 US-10-225-567A-43	Sequence 43, Appl
41	15.8	79.0	6456	13 US-10-311-455-980	Sequence 980, Appl
42	15.8	79.0	684707	12 US-10-398-221-9	Sequence 9, Appl
43	15.8	79.0	3011208	12 US-10-398-221-2058	Sequence 2058, Appl
44	15.8	79.0	3673778	13 US-10-312-841-1	Sequence 1, Appl
45	15.8	79.0	3673778	13 US-10-312-841-2	Sequence 2, Appl

ALIGNMENTS

US-10-001-073-16	US-10-001-073-16
Sequence 16, Application US/10001073	
Publication No. US20030113725A1	
GENERAL INFORMATION:	
APPLICANT: Liggett, Stephen	
APPLICANT: Small, Kirsten	
TITLE OF INVENTION: Alpha-2-adrenergic receptor polymorphisms	
FILE REFERENCE: 13073-PCT	
CURRENT APPLICATION NUMBER: US/10/001, 073	
NUMBER OF SEQ ID NOS: 53	
SOFTWARE: Patentin Ver. 2.0	
SEQ ID NO 16	
LENGTH: 20	
TYPER: DNA	
ORGANISM: Homo sapiens	
US-10-001-073-16	
Query Match	100.0%; Score 20; DB 15; Length 20;
Best Local Similarity	100.0%; Pred. No. 5.6; Mismatches 0; Indels 0; Gaps 0;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY	1 AAAAAGCCCAATGACCACAG 20
DB	1 AAAAAGCCCAATGACCACAG 20
RESULT 2	
US-09-825-923-1/c	
Sequence 1, Application US/09825923	
Patent No. US20010016338A1	
GENERAL INFORMATION:	
APPLICANT: Snapit, Amir	
APPLICANT: Heimonen, Paula	
APPLICANT: Alhopuro, Pia	
APPLICANT: Karvonen, Matti	
APPLICANT: Koulu, Markku	

APPLICANT: Pesonen, Ullamari
APPLICANT: Scheinin, Mika
APPLICANT: Salonen, Jukka T
APPLICANT: Tuomainen, Tomi-Pekka
APPLICANT: Lakka, Timo A
APPLICANT: Nyysen, Kristiina
APPLICANT: Salonen, Riitta
APPLICANT: Kaunonen, Jussi
APPLICANT: Valkonen, Veli-Pekka
TITLE OF INVENTION: A DNA molecule encoding a variant alpha-2B-adrenoceptor
FILE REFERENCE: Protein, and uses thereof
CURRENT APPLICATION NUMBER: US/09/825,923
CURRENT FILING DATE: 2001-04-05
PRIOR APPLICATION NUMBER: 09/422,985
PRIOR FILING DATE: 2000-05-25
NUMBER OF SEQ ID NOS: 10
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1
LENGTH: 1344
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (1)..(1341)
OTHER INFORMATION: Coding sequence for variant human
OTHER INFORMATION: alpha-2B-adrenoceptor protein
US-09-825-923-1

Query Match 100.0%; Score 20; DB 9; Length 1344;
Best Local Similarity 100.0%; Pred. No. 8.4;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AAAAAGCCCATGACACAG 20
DB 1131 AAAAAGCCCATGACACAG 1112

RESULT 3
US-10-077-870-1/C
Sequence 1, Application US/10077870
Publication No. US2003003470A1
GENERAL INFORMATION:
APPLICANT: Salonen, Jukka T
TITLE OF INVENTION: Method for detecting a risk of hypertension and uses thereof
FILE REFERENCE: 0933-0183P
CURRENT APPLICATION NUMBER: US/10/077,870
CURRENT FILING DATE: 2002-05-21
PRIOR APPLICATION NUMBER: FI 20010323
PRIOR FILING DATE: 2001-02-20
NUMBER OF SEQ ID NOS: 10
SOFTWARE: PatentIn Ver. 3.1
SEQ ID NO 1
LENGTH: 1344
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (1)..(1341)
OTHER INFORMATION: Coding sequence for variant human alpha-2B-adrenoceptor protein
US-10-077-870-1

Query Match 100.0%; Score 20; DB 15; Length 1344;
Best Local Similarity 100.0%; Pred. No. 8.4;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AAAAAGCCCATGACACAG 20
DB 1131 AAAAAGCCCATGACACAG 1112

RESULT 4
US-10-001-073-2/C

Sequence 2, Application US/10001073
Publication No. US20030113725A1
GENERAL INFORMATION:
APPLICANT: Liggett, Stephen
APPLICANT: Small, Kirsten
TITLE OF INVENTION: Alpha-2-adrenergic receptor polymorphisms
FILE REFERENCE: 13073-PCT
CURRENT APPLICATION NUMBER: US/10/001,073
CURRENT FILING DATE: 2001-11-01
NUMBER OF SEQ ID NOS: 53
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2
LENGTH: 1344
TYPE: DNA
ORGANISM: Homo sapiens
US-10-001-073-2

Query Match 100.0%; Score 20; DB 15; Length 1344;
Best Local Similarity 100.0%; Pred. No. 8.4;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AAAAAGCCCATGACACAG 20
DB 1131 AAAAAGCCCATGACACAG 1112

RESULT 5
US-09-825-923-3/C
Sequence 3, Application US/09825923
Patent No. US20010016338A1
GENERAL INFORMATION:
APPLICANT: Snajit, Amir
APPLICANT: Heinonen, Paula
APPLICANT: Alhopuro, Pia
APPLICANT: Karvonen, Matti
APPLICANT: Koulou, Markku
APPLICANT: Pesonen, Ullamari
APPLICANT: Scheinin, Mika
APPLICANT: Salonen, Jukka T
APPLICANT: Tuomainen, Tomi-Pekka
APPLICANT: Lakka, Timo A
APPLICANT: Nyysen, Kristiina
APPLICANT: Salonen, Riitta
APPLICANT: Kaunonen, Jussi
APPLICANT: Valkonen, Veli-Pekka
TITLE OF INVENTION: A DNA molecule encoding a variant alpha-2B-adrenoceptor
FILE REFERENCE: Protein, and uses thereof
CURRENT APPLICATION NUMBER: US/09/825,923
CURRENT FILING DATE: 2001-04-05
PRIOR APPLICATION NUMBER: 09/422,985
PRIOR FILING DATE: 2000-05-25
NUMBER OF SEQ ID NOS: 10
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 3
LENGTH: 1353
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (1)..(1350)
OTHER INFORMATION: Coding sequence for human alpha-2B-adrenoceptor
OTHER INFORMATION: protein
US-09-825-923-3

Query Match 100.0%; Score 20; DB 9; Length 1353;
Best Local Similarity 100.0%; Pred. No. 8.4;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AAAAAGCCCATGACACAG 20
DB 1140 AAAAAGCCCATGACACAG 1121

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RESULT 6
US-10-077-870-3/c
; Sequence 3, Application US/10077870
; Publication No. US20030003470A1
; GENERAL INFORMATION:
; APPLICANT: Salonen, Jukka T
; TITLE OF INVENTION: Method for detecting a risk of hypertension and uses thereof
; FILE REFERENCE: 0933-0183P
; CURRENT APPLICATION NUMBER: US/10/077, 870
; CURRENT FILING DATE: 2002-05-21
; PRIOR APPLICATION NUMBER: FI 20010323
; PRIOR FILING DATE: 2001-02-20
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 3.1
; SEQ ID NO 3
; LENGTH: 1353
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1350)
; OTHER INFORMATION: Coding sequence for human alpha-2B-adrenoceptor protein
US-10-077-870-3

Query Match      100.0%; Score 20; DB 15; Length 1353;
Best Local Similarity 100.0%; Pred. No. 8.4;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 AAAAAGCCCAATGACCACAG 20
Db      1140 AAAAAGCCCAATGACCACAG 1121

RESULT 7
US-10-001-073-1/c
; Sequence 1, Application US/10001073
; Publication No. US20030113725A1
; GENERAL INFORMATION:
; APPLICANT: Liggett, Stephen
; APPLICANT: Small, Kirsten
; TITLE OF INVENTION: Alpha-2-adrenergic receptor polymorphisms
; FILE REFERENCE: 13073-PCT
; CURRENT APPLICATION NUMBER: US/10/001, 073
; CURRENT FILING DATE: 2001-11-01
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 1353
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-001-073-1

Query Match      100.0%; Score 20; DB 15; Length 1353;
Best Local Similarity 100.0%; Pred. No. 8.4;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 AAAAAGCCCAATGACCACAG 20
Db      1140 AAAAAGCCCAATGACCACAG 1121

RESULT 8
US-10-305-720-1181/c
; Sequence 1181, Application US/10305720
; Publication No. US20040010136A1
; GENERAL INFORMATION:
; APPLICANT: Au-Yang, Janice K.; Seilhamer, Jeffrey J.
; TITLE OF INVENTION: Composition for the Detection of Signaling Pathway Gene Expression
; FILE REFERENCE: PA-0002-1 CON
; CURRENT APPLICATION NUMBER: US/10/305, 720
; CURRENT FILING DATE: 2002-11-26
; PRIOR APPLICATION NUMBER: 09/016,434

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; PRIOR FILING DATE: 1998-01-30
; NUMBER OF SEQ ID NOS: 1490
; SOFTWARE: PERL Program
; SEQ ID NO 1181
; LENGTH: 2072
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: GenBank ID No. US20040010136A1 g178197
US-10-305-720-1181

Query Match      100.0%; Score 20; DB 12; Length 2072;
Best Local Similarity 100.0%; Pred. No. 8.7;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 AAAAAGCCCAATGACCACAG 20
Db      1552 AAAAAGCCCAATGACCACAG 1533

RESULT 9
US-10-225-567A-41/c
; Sequence 41, Application US/10225567A
; Publication No. US20030113798A1
; GENERAL INFORMATION:
; APPLICANT: Lifespan Biosciences
; APPLICANT: Brown, Joseph P.
; APPLICANT: Burner, Glenna C.
; APPLICANT: Roush, Christine L.
; TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS
; FILE REFERENCE: 1920-4-4
; CURRENT APPLICATION NUMBER: US/10/225, 567A
; CURRENT FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 60/257,144
; PRIOR FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 2292
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 41
; LENGTH: 3274
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-225-567A-41

Query Match      100.0%; Score 20; DB 15; Length 3274;
Best Local Similarity 100.0%; Pred. No. 9.1;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 AAAAAGCCCAATGACCACAG 20
Db      1140 AAAAAGCCCAATGACCACAG 1121

RESULT 10
US-09-770-445-297/c
; Sequence 297, Application US/09770445
; Patent No. US2002023281A1
; GENERAL INFORMATION:
; APPLICANT: Goriach, Jorn
; APPLICANT: An, Yong-Qiang
; APPLICANT: Hamilton, Carol M.
; APPLICANT: Price, Jennifer L.
; APPLICANT: Raines, Tracy M.
; APPLICANT: Yu, Yang
; APPLICANT: Rameaka, Joshua G.
; APPLICANT: Page, Amy
; APPLICANT: Matthews, Abraham V.
; APPLICANT: Ledford, Brooke L.
; APPLICANT: Woessner, Jeffrey P.
; APPLICANT: Haas, William David
; APPLICANT: Garcia, Carlos A.
; APPLICANT: Kricker, Maaja
; APPLICANT: Slader, Ted

```

```

; APPLICANT: Davis, Keith R.
; APPLICANT: Allen, Keith
; APPLICANT: Hoffman, Neil
; APPLICANT: Hurlan, Patrick
; TITLE OF INVENTION: Expressed Sequences of Arabidopsis
; TITLE OF INVENTION: thaliana
; FILE REFERENCE: 2023US (PARA-012PRV)
; CURRENT APPLICATION NUMBER: US/09/770,445
; CURRENT FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: US 60/178,472
; PRIOR FILING DATE: 2000-01-27
; NUMBER OF SEQ ID NOS: 999
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 297
; LENGTH: 965
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(965)
; OTHER INFORMATION: n = A,T,C or G
US-09-770-445-297

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Query Match      87.0%; Score 17.4; DB 9; Length 965;
Best Local Similarity 94.7%; Pred. No. 1.4e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY      2 AAAAGCCCATGACACAG 20
Db      219 AAAAGCCCATGACACAG 201

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RESULT 11
US-10-369-493-42551/c
; Sequence 42551, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianteng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 42551
; LENGTH: 1767
; TYPE: DNA
; ORGANISM: Arabidopsis PCC7120
US-10-369-493-42551

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Query Match      84.0%; Score 16.8; DB 12; Length 1767;
Best Local Similarity 90.0%; Pred. No. 2.8e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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QY      1 AAAAAGCCCATGACACAG 20
Db      923 AAAAAGCCCATGACACAG 904

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RESULT 12
US-10-398-221-1266
; Sequence 1266, Application US/10398221
; Publication No. US20040018514A1
; GENERAL INFORMATION:
; APPLICANT: KUNST, Frederick
; APPLICANT: GLASER, Philippe
; TITLE OF INVENTION: Listeria innocua, genome and applications

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; FILE REFERENCE: 344 702 - US
; CURRENT APPLICATION NUMBER: US/10/398,221
; CURRENT FILING DATE: 2003-03-27
; PRIOR APPLICATION NUMBER: PCT/FR 01/03 061
; PRIOR FILING DATE: 2001-10-04
; PRIOR APPLICATION NUMBER: FR 00/12 697
; PRIOR FILING DATE: 2000-10-04
; NUMBER OF SEQ ID NOS: 4025
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1266
; LENGTH: 788
; TYPE: DNA
; ORGANISM: Listeria monocytogenes-4B
US-10-398-221-1266

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Query Match      82.0%; Score 16.4; DB 12; Length 788;
Best Local Similarity 94.4%; Pred. No. 4e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY      1 AAAAAGCCCATGACACAG 18
Db      244 AAAAAGCCCATGACACAG 261

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RESULT 13
US-09-738-626-743/c
; Sequence 743, Application US/09738626
; Publication No. US20020197605A1
; GENERAL INFORMATION:
; APPLICANT: NAKAGAWA, SATOSHI
; APPLICANT: MIZOGUCHI, HIROSHI
; APPLICANT: ANDO, SEIKO
; APPLICANT: HAYASHI, MIKIRO
; APPLICANT: OCHIAI, KEIKO
; APPLICANT: YOKOI, HARUHIKO
; APPLICANT: TATEISHI, NAOKO
; APPLICANT: SENOH, AKIHITO
; APPLICANT: IKEDA, MASATO
; APPLICANT: OZAKI, AKIO
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-125
; CURRENT APPLICATION NUMBER: US/09/738,626
; CURRENT FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: JP 99/377484
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: JP 00/159162
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: JP 00/280988
; PRIOR FILING DATE: 2000-08-03
; NUMBER OF SEQ ID NOS: 7059
; SOFTWARE: PatentIn ver. 3.0
; SEQ ID NO 743
; LENGTH: 996
; TYPE: DNA
; ORGANISM: Corynebacterium glutamicum
US-09-738-626-743

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Query Match      82.0%; Score 16.4; DB 10; Length 996;
Best Local Similarity 94.4%; Pred. No. 4.1e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY      3 AAAGCCCATGACACAG 20
Db      319 AAATGCCCATGACACAG 302

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RESULT 14
US-10-292-798-1745/c
; Sequence 1745, Application US/10292798
; Publication No. US20030235833A1
; GENERAL INFORMATION:
; APPLICANT: SUWA, MAKIKO
; APPLICANT: ASAI, KIYOSHI

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Job time : 122.659 seconds

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1  APPLICANT: AKIYAMA, YUTAKA
2  APPLICANT: ABRARATANI, HIROYUKI
3  TITLE OF INVENTION: GUANOSINE TRIPHOSPHATE-BINDING PROTEIN COUPLED RECEPTORS
4  FILE REFERENCE: 08435/166
5  CURRENT APPLICATION NUMBER: US/10/592,798
6  CURRENT FILING DATE: 2002-11-13
7  PRIOR APPLICATION NUMBER: 10/017,161
8  PRIOR FILING DATE: 2001-12-18
9  PRIOR APPLICATION NUMBER: JP 2001-246789
10 PRIOR FILING DATE: 2001-06-18
11 NUMBER OF SEQ ID NOS: 2070
12 SOFTWARE: PatentIn Ver. 2.1
13 SEQ ID NO 1745
14 LENGTH: 1282
15 TYPE: DNA
16 ORGANISM: Homo sapiens
17 FEATURE:
18 LOCATION: source
19 FEATURE:
20 LOCATION: (1)..(1282)
21 FEATURE:
22 NAME/KEY: CDS
23 LOCATION: (201)..(1082)
24 US-10-292-798-1745

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Best Local Similarity	99.4%	Pred. No. 4.2e+02		
Matches 17, Conservative	0	Mismatches 1	Indels 0	Gaps 0

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Qy      2  AAACGCCAATGACCACA 19
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Db      1071 ACAACGCCAATGACCACA 1054

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RESULT 15
US-10-017-161-2099/c
? Sequence 2099, Application US/10017161
? Publication No. US2003014368A1
? GENERAL INFORMATION:
? APPLICANT: SUMA, MAKIHO
? APPLICANT: ASAI, KIYOSHI
? APPLICANT: AKIYAMA, YUTAKA
? APPLICANT: ABRAYAN, HIRYUKI
? TITLE OF INVENTION: NOVEL G PROTEIN-COUPLED RECEPTORS
? FILE REFERENCE: 06435/0152
? CURRENT APPLICATION NUMBER: US/10/017.161
? CURRENT FILING DATE: 2002-12-18
? PRIOR APPLICATION NUMBER: JP 2001/246789
? PRIOR FILING DATE: 2001-06-18
? NUMBER OF SEQ ID NOS: 2430
? SOFTWARE: PatentIn Ver. 2.1
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? ORGANISM: Homo sapiens
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? NAME/KEY: source
? LOCATION: (1)..(1282)
? FEATURE:
? NAME/KEY: CDS
? LOCATION: (201)..(1082)
? US-10-017-161-2099

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Best Local Similarity	94.4%;	Pred. No. 4.2e+02;		
Matches 17;	Conservative 0;	Mismatches 1;	Indels 0;	Gaps 0;

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QY      2  AAACGCCAATGACCACA 19
          |||||
Db      1071 ACAACGCCAATGACCACA 1054

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 12, 2004, 03:54:41 / Search time 1081.71 Seconds
(without alignments)
449.373 Million cell updates/sec

Title: US-09-692-077D-16

Perfect score: 20
Sequence: 1 aaacgcgaatgaccacag 20

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 22781392 seqs, 12152238056 residues

Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: em_estba:*
2: em_estbam:*
3: em_estin:*
4: em_estm:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_hic:*
9: gb_est1:*
10: gb_est2:*
11: gb_hic:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: em_gsa_hum:*
18: em_gsa_hiv:*
19: em_gsa_pin:*
20: em_gsa_vrt:*
21: em_gsa_fun:*
22: em_gsa_mam:*
23: em_gsa_mus:*
24: em_gsa_pro:*
25: em_gsa_rtd:*
26: em_gsa_phg:*
27: em_gsa_vrl:*
28: gb_gsa1:*
29: gb_gsa2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	DB ID	Description
1	19	95.0	712 29	HGRA2BAR
2	18.4	92.0	986 10	BE788667
3	17.4	87.0	527 9	AI993504
4	17.4	87.0	971 29	CNS07DB3

5	17.4	87.0	1752 10	BF129496
6	17	85.0	464 13	BY030666
7	16.8	84.0	173 9	AI395866
8	16.8	84.0	179 28	AZ070845
9	16.8	84.0	241 28	AO106085
10	16.8	84.0	321 29	BZ664659
11	16.8	84.0	393 10	BE239439
12	16.8	84.0	424 28	AO432032
13	16.8	84.0	436 9	AI735704
14	16.8	84.0	445 9	AI243573
15	16.8	84.0	500 10	BG143944
16	16.8	84.0	513 12	BM690995
17	16.8	84.0	576 28	AZ217526
18	16.8	84.0	635 13	BQ119722
19	16.8	84.0	658 13	BQ109472
20	16.8	84.0	668 28	AZ352444
21	16.8	84.0	722 14	CB677776
22	16.8	84.0	729 9	AI055134
23	16.8	84.0	742 14	CB630921
24	16.8	84.0	765 28	AZ907242
25	16.8	84.0	788 29	DREA2CAR
26	16.8	84.0	855 13	BQ901034
27	16.8	84.0	858 28	BH270411
28	16.8	84.0	878 12	BI768763
29	16.8	84.0	882 29	HIPAC2AR
30	16.8	84.0	889 29	CNS04XDZ
31	16.8	84.0	896 29	BZ203770
32	16.8	84.0	916 29	CNS01MR6
33	16.8	84.0	926 10	BG440575
34	16.8	84.0	1115 28	BH167326
35	16.8	84.0	1136 12	BG910723
36	16.4	82.0	143 10	BG549263
37	16.4	82.0	355 9	AI859458
38	16.4	82.0	405 10	BG549863
39	16.4	82.0	455 29	CC468063
40	16.4	82.0	547 12	BM499110
41	16.4	82.0	593 9	AI619097
42	16.4	82.0	655 29	AG069974
43	16.4	82.0	670 9	AM697748
44	16.4	82.0	679 29	BZ275203
45	16.4	82.0	745 10	BG319648

ALIGNMENTS

RESULT 1
LOCUS HGRA2BAR/c
DEFINITION Shark alpha2 adrenergic receptor gene fragment probably subtype b,
genomic survey sequence.
ACCESSION AL606572
VERSION AL606572.1 GI:15591923
KEYWORDS GSS; Alpha2 adrenergic receptor gene.
SOURCE Hexanchus griseus
ORGANISM Hexanchus griseus

REFERENCE
AUTHORS Hunter,C. and Elgar,G.
TITLE Alpha2 adrenergic receptor gene
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 712)
HUNTER,C.
DIRECT SUBMISSION
SUBMITTED (14-SEP-2001) MRC Human Genome Mapping Project Resource
Centre Hinxton, Cambridge, CB10 1SB. UK Email:
biocel@hmp.mrc.ac.uk

FEATURES
source
1..712
Location/Qualifiers
/organism="Hexanchus griseus"
/mol_type="genomic DNA"

BASE COUNT 188 a 187 c 180 g 157 t
 ORIGIN /db_xref="taxon:94987"

Query Match 95.0%; Score 19; DB 29; Length 712;
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 AAAAGCCCAATGACCAAG 20
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 DB 683 AAAAGCCCAATGACCAAG 665

RESULT 2
 BE788667 986 bp mRNA linear EST 20-OCT-2000
 LOCUS 60147536F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3878433 5',
 DEFINITION mRNA sequence.
 ACCESSION BE788667
 VERSION BE788667.1 GI:10209865
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 986)
 NIH-MGC http://mgs.nci.nih.gov/.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cga@db-remail.nih.gov
 Tissue Procurement: DCTD/DTF/Gazdar
 cDNA Library Preparation: Life Technologies, Inc.
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
 http://image.llnl.gov
 Plate: LLM9642 row: g column: 10
 High quality sequence ftop: 254.
 Location/Qualifiers
 1..986
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:3878433"
 /issue_type="large cell carcinoma"
 /lab_host="DH10B (phage-resistant)"
 /clone_1b="NIH MGC 68"
 /note="Organ: lung; Vector: pCMV-SPORT6; Site 1: NCI;
 Site 2: Salt; Cloned unidirectionally. Primer: Oligo dT.
 Average insert size 1.8 kb. Library constructed by Life
 Technologies."

BASE COUNT 446 a 332 c 157 g 51 t

ORIGIN

Query Match 92.0%; Score 18.4; DB 10; Length 986;
 Best Local Similarity 95.0%; Pred. No. 2.6e+02;
 Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AAAAGCCCAATGACCAAG 20
 |||
 DB 280 AAAAGCCCAATGACCAAG 299

RESULT 3
 AI993504 527 bp mRNA linear EST 08-SEP-1999
 LOCUS 701496517 A. thaliana, Ohio State clone set Arabidopsis thaliana
 DEFINITION cDNA clone 701496517, mRNA sequence.
 ACCESSION AI993504
 VERSION AI993504.1 GI:5840409
 KEYWORDS EST.

SOURCE Arabidopsis thaliana (thale cress)
 ORGANISM Arabidopsis thaliana
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids
 / eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 REFERENCE 1 (bases 1 to 527)
 Chen J., Montoya, M., Chan, E., Mooney, M., Carroon, B., Gilliland, D.,
 Wang, X., Hillman, J., Guebler, K., Kim, C., Doyle, M., Brzoska, P.,
 Gorgone, G., Burns, D., Griffin, J., Mounounou, M., Nguyen, D., Tan, R.,
 Rose, M., Warren, B., Ton, B., Kastury, K., Borillo, C., Carpio, T.,
 Policky, J., Suzuki, G., Argentine, C., Shah, S., Nobrega, A., Murry, L.,
 Turner, C., Kikorian, S., Elder, L. and Hanson, D.
 TITLE Arabidopsis thaliana Gene Expression Microarray
 JOURNAL Unpublished
 COMMENT Contact: David Smoller, Ph.D.
 Genome Systems, Inc., a wholly owned subsidiary of Incyte
 Pharmaceuticals, Inc.
 4633 World Parkway Circle, St. Louis, MO 63134, USA
 Tel: 877-577-2733
 Fax: 314-427-3324
 Email: service@genomesystems.com.

FEATURES
 source
 1..527
 /organism="Arabidopsis thaliana"
 /mol_type="mRNA"
 /db_xref="taxon:3702"
 /clone="701496517"
 /clone_1b="A. thaliana, Ohio State clone set"
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 Arabidopsis thaliana Ohio State clone set."

BASE COUNT 121 a 163 c 115 g 128 t

ORIGIN

Query Match 87.0%; Score 17.4; DB 9; Length 527;
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 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 AAAAGCCCAATGACCAAG 20
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 DB 258 AAAAGCCCAATGACCAAG 240

RESULT 4
 CDS07D83 971 bp DNA linear GSS 08-JUL-2001
 LOCUS T3 end of clone BD0A010C06 of library BD0A from strain CBS 94 of
 DEFINITION Candida tropicalis, genomic survey sequence.
 ACCESSION AL440137
 VERSION AL440137.1 GI:12223548
 KEYWORDS GSS.
 SOURCE Candida tropicalis
 ORGANISM Candida tropicalis
 Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 Saccharomycetales; mitosporic Saccharomycetales; Candida.
 REFERENCE 1 (bases 1 to 971)
 Soucier, J.L., Aigle, M., Artiguenave, F., Blandin, G.,
 Bolotin-Fukuhara, M., Bon, B., Brotier, P., Casaregola, S.,
 de-Montigny, J., Dujon, B., Durrens, F., Leplinge, A., Llorente, B.,
 Malpertuy, A., Neuvéglise, C., Ozler-Kalogeropoulos, O., Potier, S.,
 Saurin, W., Tekala, F., Toffano-Nioche, C., Wesolowski-Louvel, M.,
 Wincker, P. and Weissenbach, J.
 TITLE Genomic exploration of the hemiascomycetous Yeasts: 1. A set of
 yeast species for molecular evolution studies
 JOURNAL FEMS Lett. 487 (1), 3-12 (2000)
 MEDLINE 20584711
 PUBMED 1152876
 REFERENCE 2 (bases 1 to 971)
 Blandin, G., Ozler-Kalogeropoulos, O., Wincker, P., Artiguenave, F. and
 Dujon, B.
 TITLE Genomic exploration of the hemiascomycetous yeasts: 16. Candida
 tropicalis
 JOURNAL FEMS Lett. 487 (1), 91-94 (2000)
 MEDLINE 20584726

PUBMED 1152891
 REFERENCE 3 (bases 1 to 971)
 AUTHORS Genoscope.
 TITLE Direct Submission
 JOURNAL Submitted (08-SEP-2000) Genoscope - Centre National de Sequencage,
 2 rue Gaston Cremieux, CP 5706, 91057 EVRY cedex, FRANCE. (E-mail :
 beqet@genoscope.cns.fr - Web :
 http://genoscope.cns.fr)

COMMENT
 This GSS is part of a random genomic sequencing program of thirteen
 yeast species: *Saccharomyces bayanus* var. *uvarum*, *Saccharomyces*
exiguus, *Saccharomyces servazzii*, *Zygosaccharomyces rouxii*,
Saccharomyces kluyveri, *Kluyveromyces thermotolerans*, *Kluyveromyces*
lactis var. *lactis*, *Kluyveromyces marxianus* var. *marxianus*, *Pichia*
angusta, *Debaryomyces hansenii* var. *hansenii*, *Pichia sorbitophila*,
Candida tropicalis and *Yarrowia lipolytica*. Genomic inserts of 3 to
 5 kb were prepared and both extremities were sequenced. See
 keywords for description of this sequence and for the sequence of
 the other extremity of this insert.

FEATURES
 Location/Qualifiers

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 /organism="Candida tropicalis"
 /mol_type="genomic DNA"
 /strain="CBS 94"
 /db_xref="taxon:5482"
 /clone="BD0A010C06"
 /clone_1b="BD0A"
 /note="end : 73"
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 Best Local Similarity 94.7%; Pred. No. 8e+02;
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AAAACGCCAATGACACCA 19
 |||||
 Db 818 AAAACGCCAATGACACCA 836

RESULT 5
 LOCUS BF129496 1752 bp mRNA linear EST 24-OCT-2000
 DEFINITION 601811063R1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4054095 3',
 mRNA sequence.
 ACCESSION BF129496
 VERSION BF129496.1 GI:10968446
 KEYWORDS EST.

SOURCE
 ORGANISM Homo sapiens (human)
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE
 AUTHORS NIH-MGC http://mgs.nci.nih.gov/
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cga@bbs-rmmail.nih.gov
 Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
 cDNA Library Preparation: Ling Hong/Rubin Laboratory
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
 http://image.llnl.gov

Plate: L1C8893 row: n column: 16
 High quality sequence start: 132
 High quality sequence stop: 163.
 Location/Qualifiers

FEATURES
 Source

1..1752
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 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:4054095"
 /tissue_type="primary B-cells from tonsils (cell line)"

/lab host="DH10B (phage-resistant)"
 /clone_1b="NIH_MGC_48"
 /note="Organ: B-cells; Vector: pOTB7; Site 1: XhoI;
 Site 2: EcoRI; cDNA made by oligo-dT priming.
 Directionally cloned into EcoRI/XhoI sites using the
 following 5' adaptor: GGACAGG(G). Size-selected >500bp
 for average insert size 1.8kb. Library constructed by Ling
 Hong in the laboratory of Gerald M. Rubin (University of
 California, Berkeley) using ZAP-cDNA synthesis kit
 (Stratagene) and Superscript II RT (Life Technologies).
 Note: this is a NIH_MGC library." 1 others

BASE COUNT 468 a 455 c 497 g 331 t
 ORIGIN

Query Match 87.0%; Score 17.4; DB 10; Length 1752;
 Best Local Similarity 94.7%; Pred. No. 9.9e+02;
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 AAAACGCCAATGACACCA 20
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 Db 251 AAAACGCCAATGACACCA 269

RESULT 6
 LOCUS BY030666/c 464 bp mRNA linear EST 06-DEC-2002
 DEFINITION BY030666 RIKEN full-length enriched, 1 cell embryo Mus musculus
 cDNA clone I0C0014E12 5', mRNA sequence.
 ACCESSION BY030666
 VERSION BY030666.1 GI:26136109
 KEYWORDS EST.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus

REFERENCE
 AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 464)
 Okazaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S.,
 Nikaido, I., Oeato, N., Saito, R., Suzuki, H., Yamana, I., Kiyosawa, H.,
 Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A., Schonbach, C.,
 Gojobori, T., Baldarelli, R., Hill, D.P., Bult, C., Hume, D.A.,
 Quackenbush, J., Schriml, L.M., Kanapin, A., Matsuda, H., Batalov, S.,
 Beisel, K.W., Blake, J.A., Brad, D., Brusc, V., Choctha, C., Coban, L.E.,
 Cousins, S., Dalla, E., Dragani, T.A., Flechard, C.F., Forrest, A.,
 Frazer, K.S., Gaasterland, T., Gariboldi, M., Gissi, C., Godzik, A.,
 Gough, J., Grimond, S., Gustincich, S., Hirokawa, N., Jackson, I.J.,
 Jarvis, E.D., Kana, A., Kawaji, H., Kawasawa, Y., Kedierski, R.M.,
 King, B.L., Konagaya, A., Kurochkin, I.V., Lee, Y., Lennard, B., Lyons, P.A.,
 Maglott, D.R., Maltais, L., Marchionni, L., McKenzie, L., Mik, H.,
 Nagashima, T., Numata, K., Okido, T., Pavan, W.J., Perlea, G.,
 Pesole, G., Petrowsky, N., Pillai, R., Pontius, J.U., Qi, D.,
 Ramchandran, S., Ravasi, T., Reed, J.C., Reed, D.J., Reid, J., Ring, B.Z.,
 Ringwald, M., Sanderlin, A., Schneider, C., Semple, C.A., Setou, M.,
 Shimada, K., Sultana, R., Takenaka, Y., Taylor, M.S., Teasdale, R.D.,
 Tomita, M., Verrardo, R., Wagner, L., Wahlestedt, C., Wang, Y.,
 Watanabe, Y., Wells, C., Wilming, L.G., Wynshaw-Boris, A., Yanagisawa, M.,
 Yang, I., Yang, L., Yuan, Z., Zavolan, M., Zhu, Y., Zimmer, A.,
 Carninci, P., Hayatsu, N., Hirozane-Kishikawa, T., Kono, H., Nakamura, M.,
 Sakazume, N., Sato, K., Shiraki, T., Waki, K., Kawai, J., Aizawa, K.,
 Aikawa, T., Fukuda, S., Hara, A., Hashizume, W., Inotani, K., Ishii, Y.,
 Itoh, M., Kagawa, I., Miyazaki, A., Sakai, K., Sasaki, D., Shibata, K.,
 Shinagawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, E.S.,
 Rogers, J., Birney, E. and Hayashizaki, Y.

TITLE
 JOURNAL
 MEDLINE
 PUBMED
 COMMENT
 Analysis of the mouse transcriptome based on functional annotation
 of 60,770 full-length cDNAs
 Nature 420, 563-573 (2002)
 12466851
 22354683
 Contact: Yoshihide Hayashizaki
 Laboratory for Genome Exploration Research Group, RIKEN Genomic
 Sciences Center (GSC), Yokohama Institute
 The Institute of Physical and Chemical Research (RIKEN)
 1-7-22 Suenho-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
 Tel: 81-45-503-9222

Fax: 81-45-503-9216
 Email: genome-res@gsic.riken.go.jp,
 URL: http://genome.gsc.riken.go.jp/
 Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Fukuda, S., Hirozane
 T., Imotani, K., Ishii, Y., Itoh, M., Kawai, J., Kono, H., Miyazaki, A.,
 Murata, M., Nakamura, M., Nomura, K., Numazaki, R., Ohno, M., Sakai, K.,
 Sakazume, N., Sasaki, D., Sato, K., Shibata, K., Shiraki, T., Tagami,
 M., Waki, K., Watabiki, A., Muramatsu, M. and Hayashizaki, Y. Direct
 Submission
 Computational Analysis of Full-length Mouse cDNAs Compared with
 Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
 Normalization and subtraction of cap-trapper-selected cDNAs to
 prepare full-length cDNA libraries for rapid discovery of new
 genes. Genome Res. 10 (10), 1617-1630 (2000)
 RIKEN integrated sequence analysis (RISA) system-384-format
 sequencing pipeline with 384 multichiparray sequencer. Genome Res.
 10 (11), 1757-1771 (2000)
 Computer-based methods for the mouse full-length cDNA
 encyclopedia: real-time sequence clustering for construction of a
 nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
 cDNA library was prepared and sequenced in Mouse Genome
 Encyclopedia Project of Genome Exploration Research Group in Riken
 Genomic Sciences Center and Genome Science Laboratory in Riken.
 Division of Experimental Animal Research in Riken contributed to
 prepare mouse tissues.
 Please visit our web site (http://genome.gsc.riken.go.jp) for
 further details.

FEATURES
 source
 Location/Qualifiers
 1. 464
 /organism="Mus musculus"
 /mol_type="mRNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="I0C0014E12"
 /cell_type="1 cell"
 /dev_stage="1 cell embryo"
 /clone_lib="RIKEN full-length enriched, 1 cell embryo"
 83 c 126 g 111 t

BASE COUNT
 144 a 144 a 83 c 126 g 111 t

ORIGIN
 144 a 144 a 83 c 126 g 111 t

Query Match 85.0%; Score 17; DB 13; Length 464;
 Best Local Similarity 100.0%; Pred. No. 9.6e+02;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY
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 |||||
 428 AAAAAGCCCATGACCA 412

Db
 428 AAAAAGCCCATGACCA 412

RESULT 7
LOCUS
 A1395866 173 bp mRNA linear EST 11-FEB-1999
DEFINITION
 MA000059b.FGR Adult worm cDNA expression library Schistosoma
 mansoni cDNA 5', mRNA sequence.
ACCESSION
 A1395866
VERSION
 A1395866.1 GI:4225413
KEYWORDS
 EST.
SOURCE
 Schistosoma mansoni
 Schistosoma mansoni
 Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea;
 Strigeida; Schistosomatidae; Schistosomatidae; Schistosoma.
REFERENCE
 1 (bases 1 to 173)
 Oliveira, G.C. and Baba, J.
 Cataloguing Schistosoma mansoni genes with expressed sequence tags
 Unpublished
 Contact: Oliveira, Guilherme
 Lab. Parasitologia Cel. e Mol.
 Centro de Pesquisas Rene Rachou - FIOCRUZ
 Av. Augusto de Lima 1715 Barro Preto, Belo Horizonte, MG, CEP 30190
 , Brazil
 Tel: 55 31 2953566
 Fax: 55 31 2952115
 Email: oliveira@renera.cpqrr.fiocruz.br

Seq primer: M13 Reverse Universal Sequencing primer.
FEATURES
 source
 Location/Qualifiers
 1. 173
 /organism="Schistosoma mansoni"
 /mol_type="mRNA"
 /strain="LE"
 /db_xref="taxon:6183"
 /sex="Mixed"
 /dev_stage="adult"
 /clone_lib="Adult worm cDNA expression library"
 /note="Vector: Uni-Zap XR vector, Stratagene (pBluescript
 SK); Site 1: EcoRI; Site 2: XhoI; library was constructed
 and excised according to the manufacturer's instructions."

BASE COUNT
 64 a 31 c 29 g 49 t

ORIGIN
 64 a 31 c 29 g 49 t

Query Match 84.0%; Score 16.8; DB 9; Length 173;
 Best Local Similarity 90.0%; Pred. No. 8.5e+02;
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY
 1 AAAAAGCCCATGACCA 20
 |||||
 140 AAAAAGCCCATGACTAAG 159

Db
 140 AAAAAGCCCATGACTAAG 159

RESULT 8
LOCUS
 A2070845 179 bp DNA linear GSS 30-MAR-2000
DEFINITION
 RPCT-23-422G2.TV RPCT-23 Mus musculus genomic clone RPCT-23-422G2,
 genomic survey sequence.
ACCESSION
 A2070845
VERSION
 A2070845.1 GI:7362097
KEYWORDS
 GSS.
SOURCE
 Mus musculus (house mouse)
ORGANISM
 Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 179)
 Zhao, S., Niernan, W., Feldblum, T., Malek, J., Shatman, S., Akimov,
 B., Levins, M., McGinn, S., Tsegaye, G., Geer, K., Krol, M., de Jong, P.
 and Fraser, C.M.
 Mouse BAC End Sequences from Library RPCT-23
 Unpublished
 Contact: Shaying Zhao
 Department of Eukaryotic Genomics
 The Institute for Genomic Research
 9712 Medical Center Dr., Rockville, MD 20850, USA
 Tel: 301 838 0200
 Fax: 301 838 0208
 Email: szhao@tigr.org
 Clones are derived from the mouse BAC library RPCT-23. For BAC
 library availability, please contact Pieter de Jong
 (pieter@dejong.med.buffalo.edu). Clones may be purchased from
 BACPAC Resources (http://bacpac.med.buffalo.edu/orderingframe.htm)
 or from Resea ch Genetics (info@resgen.com). BAC end page:
 http://www.tigr.org/tldb/bac_ends/mouse/bac_end_intro.html
 plate: 422 row: G column: 2
 Seq primer: T7
 Class: BAC ends.

FEATURES
 source
 Location/Qualifiers
 1. 179
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="RPCT-23-422G2"
 /sex="Female"
 /lab_host="DH10B"
 /clone_lib="RPCT-23"
 /note="Organ: Kidney/Brain; Vector: pBACe3.6; Site 1:
 EcoRI; Site 2: EcoRI; Female C57BL/6J mouse kidney and/or
 brain genomic DNA was isolated and partially digested

with a combination of EcoRI and EcoRI Methylase. Size selected DNA was cloned into the pBAC3.6 vector at the EcoRI sites. The ligation products were transformed into DH10B electrocompetent cells (BRL Life Technologies). "

BASE COUNT 76 a 58 c 45 g 0 t

Query Match 84.0%; Score 16.8; DB 28; Length 179;
Best Local Similarity 90.0%; Pred. No. 8.6e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AAAAGCCCATGACACAG 20
Db 78 AAAAGCCCATGACACAG 97

RESULT 9

LOCUS AQ106085 241 bp DNA linear GSS 28-AUG-1998
DEFINITION HS 3054 A1 E12 MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3054 Col=23 Row=1, genomic survey sequence.

ACCESSION AQ106085 GI:3481441
VERSION AQ106085.1
KEYWORDS GSS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
AUTHORS 1 (bases 1 to 241)
Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T., Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and Hood,L.

TITLE Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
MEDLINE 99380589
PubMed 10449764

COMMENT Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3887
Email: jwallace@u.washington.edu

Sequence Tagged Connector
Plate: 3054 row: 1 column: 23
Class: BAC ends
High quality sequence stop: 241.
Location/Qualifiers
1..241

FEATURES

source
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/clone="Plate=3054 Col=23 Row=1"
/sex="male"
/clone_lib="CIT Approved Human Genomic Sperm Library D"
/notes="Organ: Sperm; Vector: pBeloBAC11; BAC Clones in E-Coli DH10B"

BASE COUNT 52 a 54 c 52 g 83 t

Query Match 84.0%; Score 16.8; DB 28; Length 241;
Best Local Similarity 90.0%; Pred. No. 9.5e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AAAAGCCCATGACACAG 20
Db 74 AAAAGCCCATGACACAG 55

RESULT 10
B2664659/c

LOCUS B2664659 321 bp DNA linear GSS 31-JAN-2003
DEFINITION SALK_099680.45.60 x Arabidopsis thaliana TDNA insertion lines
Arabidopsis thaliana genomic clone SALK_099680.45.60.x, genomic survey sequence.

ACCESSION B2664659 GI:28181534
VERSION B2664659.1
KEYWORDS GSS.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana

REFERENCE Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids
1 (bases 1 to 321)
eucosids II; Brassicales; Brassicaceae; Arabidopsis.
Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R., Gadrihab
C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L., Shum,P., Zimmerman,J. and Ecker,J.R.

TITLE A Sequence-Indexed Library of Insertion Mutations in the Arabidopsis Genome
JOURNAL Unpublished

COMMENT Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
Email: ecker@salk.edu

This is single pass sequence recovered from the left border of TDNA. This sequence lies within an annotated exon of Atg23550. Class: TDNA tagged.
Location/Qualifiers
1..321

FEATURES

source
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/strain="Columbia 0"
/db_xref="taxon:3702"
/clone="SALK_099680.45.60.x"
/note="PCR was performed on Arabidopsis thaliana lines each of which contains one or more TDNA insertion elements. The resultant fragment for each line was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at http://signal.salk.edu/tdna_protocols.html"

BASE COUNT 91 a 40 c 86 g 104 t

Query Match 84.0%; Score 16.8; DB 29; Length 321;
Best Local Similarity 90.0%; Pred. No. 1.1e+03;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AAAAGCCCATGACACAG 20
Db 277 AAAAGCCCATGACACAG 258

RESULT 11
LOCUS B239439 393 bp mRNA linear EST 12-JUL-2000
DEFINITION EST392780 MHRP-Medicago truncatula CDNA clone pMHRP-47M19, mRNA sequence.
ACCESSION B239439
VERSION B239439
KEYWORDS EST.
SOURCE EST.
ORGANISM Medicago truncatula (barrel medic)

Medicago truncatula (barrel medic)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids
; eucosids I; Fabales; Fabaceae; Papilionoideae; Trifoliaceae;
Medicago.

REFERENCE 1 (bases 1 to 393)
Harrison,M.J., Town,C.D., Bowman,C.L., Craven,M.B., Hansen,T.S., Holt,I.E., Cho,J. and Fraser,C.M.
ESTs from phosphate-starved roots of Medicago truncatula

JOURNAL
COMMENT

Unpublished
Contact: Maria J. Harrison
Plant Biology Division
The Samuel Roberts Noble Foundation
2510 Sam Noble Parkway, Ardmore, OK 73401, USA
Tel: 580-223-5810
Fax: 580-221-7380
Email: mjharrison@noble.org
The Samuel Noble Roberts Foundation: N260974e
TIGR sequence name: WTHAU827K
More information is available at:
<http://chryseis.tamu.edu/medicago>
Seq primer: SKmod (CTA gaa cta gtc gat cc).

FEATURES

source

1..393

/organism="Medicago truncatula"

/mol_type="mRNA"

/cultivar="A17"

/db_xref="taxon:3880"

/clone="pMHRP-47M19"

/tissue_type="roots"

/dev_stage="phosphate-starved"

/lab_host="XLOLR"

/clone_lib="MHRP-"

/note="Vector: pluescript SK-, Site_1: EcoRI, Site_2: XhoI; At the trifoliolate stage, M. truncatula plants were transplanted to phosphate-free sand and grown for a further 30 days. During this period, they were fertilized twice weekly with 1/2 Hoaglands solutions containing 20mM potassium phosphate. cDNA was prepared from polyA-enriched RNA. The cDNA was directionally ligated into the Unizap XR vector from Stratagene and packaged using GigaPack III Gold packaging extracts. Plasmids containing cDNA inserts were excised from the recombinant lambda-Zap phage using Ex-assist helper phage and propagated in XLOLR cells."

BASE COUNT
ORIGIN

98 a 69 c 82 g 144 t

Query Match 84.0%; Score 16.8; DB 10; Length 393;
Best Local Similarity 90.0%; Pred. No. 1.1e+03;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 AAAAAGCCCAATGACCCAG 20
Db 241 AAAAAGCCCAATGACCCAG 222

RESULT 12 424 bp DNA linear GSS 31-MAR-1999
AO432032 HS_2270_A2_E11_T7C CIT Approved Human Genomic Sperm Library D Homo
LOCUS sapiens genomic clone Plate=2270 Col=22 Row=I, genomic survey
DEFINITION
sequence.

ACCESSION AO432032
VERSION AO432032.1
KEYWORDS GI:4542367
SOURCE GSS.

ORGANISM Homo sapiens (human)
Homo sapiens

REFERENCE 1 (bases 1 to 424)
AUTHORS Mahatras,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and
Hood,L.
Title: Sequence-tagged connectors: A sequence approach to mapping and
scanning the human genome
Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)

TITLE
JOURNAL
MEDLINE
PUBMED
COMMENT

Contact: Mahatras GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington

401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
Clones may be purchased from Research Genetics (info@resgen.com).
BAC end Web Server: <http://www.htsc.washington.edu>
Plate: 2270 row: I column: 22
Seq primer: T7
Class: BAC ends
High quality sequence stop: 424.

FEATURES

source

1..424

/organism="Homo sapiens"

/mol_type="genomic DNA"

/db_xref="taxon:9606"

/clone="Plate=2270 Col=22 Row=I"

/sex="male"

/clone_lib="CIT Approved Human Genomic Sperm Library D"

/note="Organ: sperm; Vector: pBelobAC11; BAC Clones in
E-Coli DH10B"BASE COUNT
ORIGIN

120 a 87 c 81 g 129 t 7 others

Query Match 84.0%; Score 16.8; DB 28; Length 424;
Best Local Similarity 90.0%; Pred. No. 1.2e+03;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 AAAAAGCCCAATGACCCAG 20
Db 196 AAAAAGCCCAATGACCCAG 215

RESULT 13 436 bp mRNA linear EST 14-JUN-1999
AI735704/c at20d01.x1 Barstead aorta HPLRB6 Homo sapiens cDNA clone
LOCUS IMAGE:2355649 3' similar to gp:M58458 40S RIBOSOMAL PROTEIN S4, X
DEFINITION
ISOFORM (HUMAN); mRNA sequence.

ACCESSION AI735704
VERSION AI735704.1
KEYWORDS GI:5057228
SOURCE EST.

ORGANISM Homo sapiens (human)
Homo sapiens

REFERENCE 1 (bases 1 to 436)
AUTHORS Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S.,
Krizman,D., Kucada,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin
J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theisling,B.,
White,Y., Wyllie,T., Waterston,R. and Wilson,R.
WashU-NCI human EST Project

Unpublished
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LINT; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -400p from Gldco
High quality sequence stop: 1.

FEATURES

source

1..436

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:2355649"

/sex="male"

/dev_stage="adult, age 64"

/lab_host="DH10B (phage resistant)"

/clone_lib="Barstead aorta HPLRB6"

/note="Organ: aorta; Vector: pT73D-Pac (Pharmacia) with a

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